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UTILITY PATENT APPLICATION TRANSMITTAL UNDER 37 CFR §1.53(b)	
Attorney Docket Number	01997/521003
Applicants	Rajesh Ranganathan, H. Robert Horvitz, and Stephen C. Cannon
Title	A NOVEL SEROTONIN-GATED ANION CHANNEL

PRIORITY INFORMATION:

This application is a continuation-in-part of and claims priority from United States patent application 09/559,622, filed April 27, 2000, which claims priority from U.S. Provisional Application Serial Number 60/131,149, filed April 27, 1999.

APPLICATION ELEMENTS:

Cover sheet	1 page
Specification	50 pages
Claims	4 pages
Abstract	1 page
Drawing	23 sheets
Combined Declaration and POA, which is: ☒ Unsigned; ☐ Newly signed for this application; ☐ A copy from prior application [**SERIAL NUMBER**] and the entire disclosure of the prior application is considered as being part of the disclosure of this new application and is hereby incorporated by reference therein.	3 pages
Statement Deleting Inventors	0 pages
Sequence Statement	0 pages
Sequence Listing on Paper	0 pages
Sequence Listing on Diskette	0 disk
Small Entity Statement, which is: ☐ Unsigned; ☐ Newly signed for this application; ☐ A copy from prior application [SERIAL NO.] and such small entity status is still proper and desired.	0 pages
Preliminary Amendment	0 pages

IDS	0 pages
Form PTO 1449	0 pages
Cited References	0 references
Recordation Form Cover Sheet and Assignment	0 pages
Assignee's Statement	0 pages
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Basic Filing Fee: $710	$710.00
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APPLICATION

FOR

UNITED STATES LETTERS PATENT

APPLICANTS: Rajesh Ranganathan, H. Robert Horvitz, and Stephen C. Cannon

TITLE: A NOVEL SEROTONIN-GATED ANION CHANNEL

A NOVEL SEROTONIN-GATED ANION CHANNEL

Cross Reference to Related Applications

This application is a continuation-in-part application of U.S.S.N. 09/559,622, filed April 27, 2000, which claims priority from U.S. Provisional Application Serial Number 60/131,149, filed April 27, 1999.

Statement as to Federally Sponsored Research

This research has been funded by NIH Grant R37GM24663. The U.S. government has certain rights to the invention.

Background of the Invention

The invention relates to the diagnosis and treatment of conditions associated with serotonin-mediated cellular responses.

The biogenic amine serotonin plays a role in the modulation of neuronal synaptic events as well as non-neuronal cellular signaling. Serotonin acts by binding to receptors on a variety of cells. These receptors fall into two broad functional and structural categories, those acting through G-proteins to mediate intracellular signaling, and those that form ion channels. It is generally believed that serotonin may act by binding to either G-protein-coupled seven-pass transmembrane receptors, or serotonin-gated cation channels. There are six major classes of G-protein-coupled receptors, each with numerous subtypes. Thus far, there is only one class of serotonin-gated ion channels, the 5-HT_3 receptor.

G-protein-coupled responses can be either excitatory or inhibitory upon activation by serotonin. Activation of G-protein-coupled receptors by serotonin generally mediates responses which are slower-acting and longer-lasting, while ion channels mediate fast-acting and transitory responses. The 5-HT_3 receptor, comprised of the conducting subunit, 5-HT_{3a} and a regulatory subunit, 5-HT_{3b}, appears to exclusively elicit excitatory responses that are generally fast-acting and transitory.

The 5-HT_3 receptor is selectively permeable to cations only, such as Na^+or K^+, and is very slightly permeable to Ca^{2+}. The influx of cations, such as Na^+ into a cell results in depolarization and excitatory neurotransmission. Efflux of cations, such as K^+ hyperpolarizes the cell, thereby reducing the likelihood of excitation, and generally leads to inhibitory neurotransmission. Since the resting membrane of a typical cell/neuron is much less permeable to Na^+ influx than to K^+ efflux, the opening of a non-selective Na^+/K^+ channel, such as the 5-HT_3 receptor leads to a dramatic influx of Na^+, leading to depolarization and excitation.

Serotonin has been implicated in the etiology of many disease states, including depression, panic disorders, obsessive compulsive disorder, cardiac abnormalities, sleep disorders, eating disorders, nausea and vomiting, gastrointestinal cramps, and migraines. G-protein-coupled serotonin receptors have been implicated in the control of mood (5-HT_{1A}), migraine (5-HT_{1B}), pain perception (5-HT_{1D}), smooth muscle contraction (5-HT_{2A}, 5-HT_7), anxiety (5-HT_{2C}), and nausea (5-HT_4). Activation of the 5-HT_3 receptor by serotonin can either stimulate or inhibit cardiac function, induce vasodilation, affect lung and intestinal function, cause pain and sensitization of nociceptive neurons, and induce nausea and vomiting. Not surprisingly, many treatments for these disorders are thought to act through serotonergic pathways.

Several classes of drugs thought to modulate the serotonergic pathway exist. For example, selective serotonin re-uptake inhibitors (SSRIs) are used to treat depression. These antidepressants, including Prozac, Zoloft, and Paxil, are believed to act by potentiating serotonin levels at the synapse. Drugs, such as Imitrex, used to treat migraine headaches, act as selective serotonin receptor agonists. Other groups of drugs used to affect mood include monoamine oxidase inhibitors, and selective serotonin receptor antagonists.

While these drugs are administered to humans to treat the above-described disease states, the patients often unpredictably experience a number of side-effects including insomnia, anxiety, chest pain, hypertension, nausea, anorexia, sweating, chills, vomiting, diarrhea, constipation, decreased libido, and abnormal ejaculation. It has been hypothesized that the side-effects result from multiple receptor activation or inactivation when a serotonin agonist or antagonist is given as a treatment. Some of these improperly activated or inactivated receptors may lead to fast- or slow-acting excitatory responses, or slow-acting inhibitory responses, when really only one specific type of response is desired.

A better understanding of serotonin-associated cellular communication could greatly facilitate the discovery of drugs and therapeutic methodologies to treat a broad range of conditions with fewer of the serious and variable side-effects prevalent with currently available drugs that interface with the serotonin pathway. Exactly how the currently available drugs that interface with the serotonin pathway work is not well understood. Agonists, antagonists, and especially serotonin re-uptake inhibitors could affect numerous serotonin receptor subtypes, and the final outcome may be a combined readout of all these varied, and sometimes antagonistic, pathways. It has been hypothesized that the various undesirable side-

effects of a given drug's action are the result of unwanted activation of the serotonin pathways that are not specific to the condition being treated. Therefore, compounds with a greater specificity for a specific serotonin receptor, for a limited subset of serotonin receptors, or for a specific subtype of a particular class of serotonin receptors would be invaluable to the field of therapeutics for serotonin-mediated disease states.

Summary of the Invention

We have discovered a serotonin-gated ion channel, MOD-1, that is exclusively permeable to chloride ions, and is not permeable to sodium, potassium, or calcium ions. Activation of this anion channel is most likely to result in an inhibitory response. In some circumstances that are dependent on the reversal potential for chloride (which is a function of the concentration of chloride inside and outside the cell) activation of anion channels could result in an excitatory response. Therefore, it is conceivable that activation of a serotonin-gated anion channel could also result in excitatory neurotransmission.

With the discovery of MOD-1 and the serotonin-gated anion channel that it forms, comes the realization that serotonin may mediate fast-acting, and transitory, inhibitory responses in addition to excitatory responses. It is possible that the activation/inactivation of a MOD-1-like serotonin-gated anion channel, in humans, is associated with some of the effects and/or side-effects of existing serotonin-based drugs. It is also conceivable that many of the serotonin-related diseases are exclusively due to defects in, or associated with, a serotonin-gated anion channel. None of the currently available drugs have been designed to effectively and specifically target this receptor. Therefore, the discoveries of a

serotonin-gated anion channel and the gene that encodes it are invaluable tools for use in discovering diagnostic and therapeutic compounds for the detection and treatment of conditions associated with serotonin-mediated cellular responses.

One way in which a serotonin-gated anion channel can be used as a tool in drug discovery is by screening existing drugs or drug candidates for their effects on serotonin-gated anion channel activity. Such an experiment can be done using MOD-1 or other serotonin-gated anion channels from non-mammals, such as nematodes, or from lower mammals or humans. Understanding how drugs affect, or do not affect, this anion channel will lend better insight into the overall effect of a drug's mechanism of action. Also, a better understanding of how this serotonin-gated anion channel is regulated will contribute to a better understanding of how current therapies work. Furthermore, information gained from this screen will permit the development of drugs with higher specificities for a particular type of serotonin-binding receptor that will mediate only the desired response. Such drugs include those which do not activate a serotonin-gated anion channel, but do activate other serotonin receptors; those that act specifically on a serotonin-gated anion channel, but not on other serotonin receptors; or those that activate a subset of the various serotonin receptors.

Methods of drug discovery are not limited to screening available drugs only, but also to all compounds and their derivatives that were extracted or synthesized during the development of a given drug affecting serotonin-mediated cellular processes. Furthermore, a *de novo* screen of chemicals can be conducted, with no bias regarding possible functional relevance, for effects on this class of serotonin-gated anion channels.

In a first aspect, the invention features a substantially pure polypeptide that is a serotonin-gated anion channel. In one embodiment, the polypeptide is a substantially pure serotonin-gated anion channel that is permeable to chloride ions. In another embodiment, the polypeptide is MOD-1. In a further embodiment, the polypeptide is a subunit that makes up a multi-subunit serotonin-gated anion channel, permeable to chloride ions. Preferably this polypeptide is from *Caenorhabditis elegans* (*C. elegans*). More preferably this polypeptide is mammalian. Most preferably this polypeptide is human.

In still another embodiment of the invention, the serotonin-gated anion channel is activated by a lower concentration of serotonin than that required to activate the 5-HT_3 receptor. For example, the serotonin-gated anion channel may have a higher binding affinity for serotonin than the 5-HT_3 receptor. This higher affinity can be assessed by calculating and comparing the dissociation constants of serotonin binding to the 5-HT_3 receptor and to a serotonin-gated anion channel.

In another aspect, the invention features a substantially pure nucleic acid sequence encoding a serotonin-gated anion channel. In one embodiment, the substantially pure nucleic acid sequence encodes a serotonin-gated anion channel that is permeable to chloride ions. In another embodiment, the nucleic acid sequence is *mod-1,* and encodes the MOD-1 polypeptide. Preferably this nucleic acid sequence is from *C. elegans*. More preferably the nucleic acid sequence is mammalian. Most preferably the nucleic acid sequence is human.

In another aspect, the invention features an antibody that preferably specifically binds to a serotonin-gated anion channel. In one embodiment, the antibody binds to a serotonin-gated anion channel that is permeable to chloride ions. This invention includes polyclonal, as well as monoclonal antibodies to the

serotonin-gated anion channel.

In another aspect, the invention features a *C. elegans* strain having a mutant *mod-1* gene. In one embodiment of the invention, the *C. elegans* strain has a mutant *mod-1* gene that does not function as a chloride channel. In another embodiment, the strain has a mutant *mod-1* gene that acts in a dominant-negative manner. In another embodiment, the strain has a mutant *mod-1* gene that encodes a polypeptide that is constitutively active.

In another aspect, the invention features a method for identifying a compound that modulates the biological activity of a serotonin-gated anion channel. The method includes the steps of: (a) administering a test compound to a serotonin-gated anion channel, and (b) assaying a modulation in the biological activity of a serotonin-gated anion channel. Assaying the modulation of biological activity may be done by measuring the current carried through a channel, or by measuring the amount of serotonin binding to a serotonin-gated anion channel. The assay can also be a bioassay that involves measuring the rate of locomotion in nematodes having a serotonin-gated anion channel. In one embodiment, the serotonin-gated anion channel is from nematodes. In another embodiment, the serotonin-gated anion channel is from a rat, mouse, or human, and is inserted into a *C. elegans* that either has or does not have a wild-type *C. elegans* serotonin-gated anion channel. In another embodiment, the serotonin-gated anion channel is a chimeric molecule between the serotonin-gated anion channels from various species. In further various embodiments of this aspect, the channel is in a cell, for example, a neuron or a non-neuronal cell. The channel may also be in a lipid bi-layer, a mammal, or a nematode. In yet another embodiment, the serotonin-gated anion channel comprises sufficient MOD-1 protein to form a serotonin-gated anion

channel.

In the above aspect of the invention, the test compound is administered in the absence or presence of serotonin, and is administered prior to, simultaneously with, or after administration of serotonin. Administration may also be in the absence or presence of known drugs that interface with the serotonin pathway. The modulation of the biological activity may be either agonistic or antagonistic. The compound may also be a cell lysate, or isolated from a cell lysate, and may be administered prior to, simultaneously with, or after administration of serotonin, or any known effector of serotonin-mediated cellular processes.

In another aspect, the invention features a method for treating a condition in a patient by administering an agonist or antagonist of a serotonin-gated anion channel to the patient. Conditions that are treated include migraine headaches, loss of appetite, gain of appetite, insomnia, inability to wake up, memory loss, inability to learn, nausea and vomiting, gastrointestinal cramps, body temperature deregulation, moods, including depression or mania, abnormal sexual or hallucinogenic behavior, abnormal cardiovascular function, abnormal muscle contraction, and abnormal endocrine regulation.

In another aspect, the invention features a diagnostic probe for measurement of a serotonin-gated anion channel, either wild-type or mutant, for detecting conditions associated with serotonin-mediated cellular responses. Measurement of a serotonin-gated anion channel includes, but is not limited to detection of nucleic acid levels that code for a serotonin-gated anion channel, levels of a polypeptide that can function as a serotonin-gated anion channel, single strand confirmation polymorphism analyses, or the flow of current across a

membrane. In one embodiment, the probe is a nucleic acid sequence that encodes a serotonin-gated anion channel, for example, MOD-1, or a polypeptide that is a serotonin-gated anion channel, or an antibody that binds to a serotonin-gated anion channel. In yet another embodiment, the probe is standard electrophysiology voltage clamping equipment that measure the activity of a serotonin-gated anion channel. In still another embodiment, the diagnostic probe is used for pharmacogenetics, i.e., in the analyses of conditions associated with serotonin-mediated cellular responses within an individual, family, or families.

In another aspect, the invention features a method for characterizing drugs associated with serotonin-mediated cellular responses, by measuring serotonin-gated anion channel activity upon drug exposure. The drugs include those already currently available for the treatment of serotonin-mediated responses, as well as small molecules that are similar in structure to these drugs. This invention also includes the discovery of any compounds which have not yet been identified as therapeutic for serotonin-mediated cellular responses.

In another aspect, the invention features a method for decreasing serotonin-gated anion channel function by decreasing the level of a serotonin-gated anion channel polypeptide with antisense RNA to the serotonin-gated anion channel, and the antisense RNA itself. Preferably the level of the serotonin-gated anion channel is deceased at least 25%, more preferably at least 50%, 70%, or 80%, and most preferably at least 95%, compared to a control (e.g., a serotonin-gated anion channel that is not contacted with an antisense RNA, or that is contacted with a nonsense RNA sequence). In addition, preferably the antisense RNA is antisense *mod-1* RNA. Such nucleic acids of the invention and methods for using them may be identified according to a method involving: (a) providing a

cell sample; (b) introducing by transformation into the cell sample, a test nucleic acid sequence for a serotonin-gated anion channel; (c) expressing the test nucleic acid of a serotonin-gated anion channel within the cell sample; and (d) determining whether the cell sample exhibits altered serotonin-gated anion channel activity, whereby either increased or decreased channel activity identifies a nucleic acid which may be used to alter serotonin-gated anion channel function. Preferably the cell is a non-neuronal cell. Most preferably the cell is a neuronal cell.

In another aspect, the invention features a method for decreasing the function of a serotonin-gated anion channel by administering an antibody that specifically binds to a serotonin-gated anion channel, or binds to a peptide from that channel. This method includes, but is not limited to, using an antibody to MOD-1 as the antibody, and a channel formed by any MOD-1 polypeptide as the channel whose function is inhibited. The methods also includes using a mammalian antibody to decrease the function of a mammalian serotonin-gated anion channel. This method also includes administration of the antibody *in vivo* or *in vitro*.

In another aspect, the invention features a method for modulating serotonin-gated anion channel activity using a nucleic acid vector encoding a serotonin-gated anion channel, and administering enough vector to alter activity of the serotonin-gated anion channels of at least one cell. In one embodiment, the vector is operably linked to a promoter. In other embodiments, the vector encodes a wild-type serotonin-gated anion channel or a mutant serotonin-gated anion channel. The mutant serotonin-gated anion channel may include, but is not limited to, a mutant channel that is a loss-of-function mutant, a dominant negative mutant, or a constitutively active mutant. In a preferred embodiment, the nucleic acid

vector encodes a wild-type or mutant MOD-1 polypeptide. In other embodiments, administration may occur *in vitro* or *in vivo*. In further embodiments, the vector encodes a polypeptide that affects the function of a serotonin-gated anion channel, or that affects molecules that are targeted subsequent to activation of a serotonin-gated anion channel. These molecules include, but are not limited to, protein kinases, protein phosphatases, and proteases.

In another aspect, the invention features a method for testing a patient having a serotonin-mediated condition, for his/her pre-disposition to respond to therapy, or to experience side-effects due to administration of a specific therapy. The method comprises:

(a) determining the characteristics of a serotonin-gated anion channel from tissues of the patient, where the characteristics are indicative of the abnormal activity of a serotonin-gated anion channel; and

(b) administering to the patient a suitable therapeutic agent relative to the degree of abnormal activity of the serotonin-gated anion channel in step (a).

In various embodiments, the abnormal activity is due to mutations in a serotonin-gated anion channel protein, altered levels of synthesis of mRNA of a serotonin-gated anion channel, altered serotonin-gated anion channel protein levels in tissues. In another embodiment, the method further comprises characterizing other serotonin-mediated receptors in the patients. Therapeutic agents to be used in accordance with the present invention may be selected from the group consisting of inhibitors or activators of serotonin-mediated pathways, including therapeutics which are currently available, as well as those which are discovered,

as described herein.

In accordance with the present invention, there is provided a method for the identification of a patient possessing a serotonin-mediated condition to be responsive to therapies for the condition, or to experience side-effects due to administration of a specific therapy. This method comprises:

(a) determining the characteristics of a serotonin-gated anion channel gene allele in a biological sample of the patient directly, using appropriate probes to a serotonin-gated anion channel, or indirectly, by phenotyping, and;

(b) correlating the genotype or phenotype with appropriated drug and/or dosage.

The presence or absence of a specific serotonin-gated anion channel allele indicates a predisposition, or lack thereof, to respond to serotonin-mediated therapies.

In another aspect, the invention claims a method for identifying a gene that is structurally related to a serotonin-gated anion channel. This method involves identifying a gene by designing probes or primers, including degenerate oligonucleotides, to specific sequences. These primers or probes encode structurally significant amino acid sequence (e.g., the sequence that forms the transmembrane portions of the serotonin-gated anion channel), and are used to screen large genomic or cDNA libraries. If a PCR approach is utilized, the primers are optionally designed to allow cloning of the amplified product into a suitable vector. PCR is particularly useful for screening cDNA libraries from rare tissue types. The method also includes identifying a gene using antibodies, using nucleic acid or amino acid scanning databases and computer programs, and screening for

genes that function in a manner similar to, or different from, a serotonin-gated anion channel.

In a related aspect, the invention features the nucleic acid sequence identified by the method of identifying a gene which is structurally related to a serotonin-gated anion channel. This gene may be isolated from nematodes or mammals, preferably from rodents, and most preferably from human.

In another aspect, the invention features a transgenic, or other mutant animal, that over-expresses or under-expresses a serotonin-gated anion channel, or expresses a dominant-negative serotonin-gated anion channel. The invention includes a nematode or a non-human mammal, for example, a mouse, as the animal. In one embodiment, the animal over-expresses a serotonin-gated anion channel that is constitutively active.

In two additional aspects, the invention features a transgenic animal and methods of using the animal for the detection of therapeutics for conditions associated with serotonin-mediated cellular responses. Preferably the animal over-expresses a serotonin-mediated anion channel polypeptide, either wild-type or mutant, or expresses an antisense RNA to a serotonin-gated anion channel or a serotonin-gated anion channel fragment. In one embodiment, the animal also has a genetic predisposition to conditions associated with serotonin-mediated cellular responses.

In yet another aspect, the invention features a method for identifying a compound that modulates the activity of a serotonin-gated anion channel by exposing a nematode to a test compound, assaying the rate of locomotion, and comparing the locomotion rate to that of a nematode receiving no test compound, serotonin, or a placebo, where a modulation in the rate of locomotion indicates a

compound that modulates the activity of a serotonin-gated anion channel. The test compound may be applied at various concentrations. In addition, the nematodes used in the screen may be bacterial-lawn deprived prior to beginning the screen.

In still another aspect, the invention features a method for identifying a compound that modulates the activity of a serotonin-gated anion channel. The method involves exposing a nematode to a test compound, quantifying the number of nematodes actively swimming after exposure to the compound, and comparing that number to that of a control receiving no test compound, serotonin, or a placebo, where a modulation in the number of actively swimming nematodes indicates a compound that modulates the activity of a serotonin-gated anion channel. The test compound may be applied at various concentrations. In addition, the nematodes used in the screen may be bacterial-lawn deprived prior to beginning the screen.

By "treatment" is meant the submission or subjection of an animal, cell, lysate or extract derived from a cell, or molecule derived from a cell to a test compound or stimulus to a serotonin-mediated response.

By a "test compound" is meant a chemical, be it naturally-occurring or artificially-derived, that is surveyed for its ability to modulate serotonin-mediated cellular responses, by employing one of the assay methods described herein. Test compounds may include, for example, peptides, polypeptides, synthetic organic molecules, naturally occurring organic molecules, nucleic acid molecules, and components thereof.

By "treat" is meant to submit or subject an animal, cell, lysate or extract derived from a cell, or molecule derived from a cell to a test compound or stimulus to a serotonin-mediated response.

By a "substantially pure polypeptide" is meant a polypeptide that has been separated from the components that naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably the polypeptide is a serotonin-gated anion channel polypeptide that is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, pure. A substantially pure serotonin-gated anion channel polypeptide may be obtained, for example, by extraction from a natural source (e.g., a neuronal or smooth muscle cell), by expression of a recombinant nucleic acid encoding a serotonin-gated anion channel polypeptide, or by chemically synthesizing the protein. Purity can be assayed by any appropriate method, e.g., by column chromatography, polyacrylamide gel electrophoresis, agarose gel electrophoresis, optical density, or HPLC analysis.

A protein is substantially free of naturally associated components when it is separated from those contaminants which accompany it in its natural state. Thus, a protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be substantially free from its naturally associated components. Accordingly, substantially pure polypeptides include those derived from eukaryotic organisms but synthesized in *E. coli* or other prokaryotes.

By a "purified nucleic acid" is meant a nucleic acid that is free of the genes which, in the naturally-occurring genome of the organism from which the nucleic acid of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant DNA that is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a

prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes recombinant DNA that is part of a hybrid gene encoding additional polypeptide sequence.

By a "serotonin-gated anion channel" is meant a channel whose opening is regulated by serotonin binding to the channel. The opening of the channel selectively permits passage of anions from one side of the channel to the other. In one embodiment, the anion is chloride. Preferably the nucleic acid sequence encoding a serotonin-gated anion channel hybridizes to a *mod-1* nucleic acid sequence.

By a "*mod-1* gene" is meant a gene encoding a polypeptide that is a serotonin-gated anion channel. In one embodiment, the *mod-1* gene is from *C. elegans*.

By a "MOD-1 protein" or "MOD-1 polypeptide" is meant a polypeptide or fragment thereof, encoded by the *mod-1* gene. In one embodiment, the MOD-1 protein or polypeptide is from *C. elegans*.

By "specifically binds" is meant an antibody that recognizes and binds to a serotonin-gated anion channel, but which does not substantially recognize and bind to other molecules in a sample, e.g., a biological sample that naturally includes other proteins.

By "mutant" is meant different from what normally appears, occurs, or functions. As used herein, the term refers to a nucleic acid sequence that is different from the wild-type sequence. This term also describes a protein encoded by the mutant nucleic acid sequence. The term also means an organism that contains a mutant nucleic acid sequence.

By "biological activity" is meant functional events mediated by a protein. In some embodiments, this includes events assayed by measuring the influx of ions into or out of a cell, or assaying the amount of serotonin binding to a channel. It also includes interactions of a polypeptide with another polypeptide. It also includes events that modify behavior or behavioral states. Such behavior includes, but is not limited to, movement, sexual behavior, or hallucinogenic behavior. Such behavioral states include, but are not limited to, migraine headaches, loss of appetite, gain of appetite, insomnia, inability to wake up, memory loss, nausea or vomiting, gastrointestinal cramps, ability or inability to learn, body temperature deregulation, moods, such as depression or mania, abnormal cardiovascular function, abnormal muscle contraction, and abnormal endocrine regulation.

As used herein, by "modulates" is meant increasing or decreasing the biological activity. Preferably the biological activity is increased or decreased 10% relative to a control. More preferably the biological activity is increased or decreased 50% relative to a control. Most preferably the biological activity is increased or decreased 90% relative to a control.

By "assaying" is meant analyzing the effect of a treatment or exposure, be it chemical or physical, administered to a whole animal or cells derived therefrom. The material being analyzed may be an animal, a cell, a lysate or extract derived from a cell, or a molecule derived from a cell. The analysis may be, for example, for the purpose of detecting current flow across a membrane, the rate of locomotion of an animal, altered gene expression, altered nucleic acid stability (e.g., mRNA stability), altered protein stability, altered protein levels, or altered protein biological activity. The means for analyzing may include, for

example, recording current changes under voltage-clamp, voltage changes in current-clamp, or extracellular potentials, counting movements of an animal under a dissecting microscope, nucleic acid amplification techniques, reporter gene assays, antibody labeling, immunoprecipitation and phosphorylation assays, and other techniques known in the art for conducting the analyses of the invention.

By "neuron" is meant a cell of ectodermal embryonic origin derived from any part of the nervous system of an animal. Neurons express well-characterized neuron-specific markers that include neurofilament proteins, MAP2, and class III β-tubulin. Included as neurons are, for example, hippocampal, cortical, midbrain dopaminergic, motor, sensory, sympathetic, septal cholinergic, and cerebellar neurons.

As used herein, by "measuring" is meant assessing an anion channel activity. Measuring can be done by use of standard electrophysiology voltage-clamping or patch-clamping equipment.

By "condition" is meant a state of being or feeling. Conditions include, but are not limited to, migraine headaches, loss of appetite, gain of appetite, insomnia, inability to wake up, memory loss, nausea or vomiting, gastrointestinal cramps, ability or inability to learn, body temperature deregulation, moods, such as depression or mania, abnormal sexual or hallucinogenic behavior, abnormal cardiovascular function, abnormal muscle contraction, and abnormal endocrine regulation.

By "promoter" is meant a minimal sequence sufficient to direct transcription of an operably-linked gene.

By "operably linked" is meant that a gene and one or more regulatory sequences are connected in such a way as to permit gene expression when the

appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences.

By "dominant-negative" is meant a nucleic acid sequence encoding a polypeptide which when expressed acts in a way to inhibit another polypeptide. This term also refers to the polypeptide itself. In one embodiment, the polypeptide that is inhibited is a wild-type polypeptide, and the dominant negative sequence encodes a mutant polypeptide of the same gene.

As referred to herein, by "constitutively active" is meant a nucleic acid sequence that encodes a polypeptide, which when expressed is in an active form at least as, or more often as the wild-type polypeptide is, in a cell in which wild-type polypeptide is naturally expressed. The polypeptide may be in an active form by being phosphorylated, or dephosphorylated, or cleaved from a propeptide to a peptide, or being ligand independent, or being mutated.

By "transgenic" is meant any cell or organism that includes a DNA sequence (transgene) that is inserted by artifice into a cell and becomes part of the genome of the organism that develops from that cell. As used herein, the transgenic organism is generally a transgenic non-human mammal (e.g., rodents such as rats or mice) or invertebrate (e.g., *Caenorhabditis elegans*).

By "antisense" is meant a nucleic acid sequence, regardless of length, that is complementary to the coding strand gene encoding a serotonin-gated anion channel. Preferably the antisense nucleic acid is capable of decreasing the activity of a serotonin-gated anion channel when present in a cell that normally is modulated by serotonin. Preferably the decrease is at least 10%, relative to a control, more preferably 25%, and most preferably 95%.

By "expose" is meant to allow contact between an animal, cell, lysate or extract derived from a cell, or molecule derived from a cell, and a test compound or activator of a serotonergic response.

By "characteristics" is meant properties or features. Characteristics include, but are not limited to, the nucleic acid sequence of a gene, or various alleles of a gene, the amino acid sequence of a protein, the level of expression of proteins or mRNA, and altered protein levels in tissues.

By "inhibit" is meant to decrease the level of expression of a serotonin-gated anion channel, or to decrease the function or activity of a serotonin-gated anion channel. Preferably the expression, function, or activity of the channel is deceased at least 25%, more preferably at least 50%, 70%, or 80%, and most preferably at least 95%, compared to a control (e.g., one which is not contacted with a test compound or an antisense nucleic acid).

Brief Description of the Drawings

Fig. 1 shows the genomic sequence of *C. elegans mod-1* (SEQ ID NO: 1).

Fig. 2 shows the cDNA sequence encoding the *C. elegans* MOD-1 polypeptide (SEQ ID NO: 2).

Fig. 3 shows the *C. elegans* MOD-1 predicted amino acid sequence (SEQ ID NO: 3).

Fig. 4 shows the structure of the *C. elegans mod-1* cDNA.

Fig. 5 is a map of the *C. elegans* strain carrying the ok103 mutation at the *mod-1* locus. The ok103 mutation is a 4135 base pair deletion in the *mod-1* genomic locus.

Fig. 6 shows the genomic sequence of the *C. elegans mod-1* gene with the ok103 mutation (SEQ ID NO: 4).

Fig. 7 shows the genomic sequence of the *C. elegans mod-1* gene with the n3034 mutation (SEQ ID NO: 5).

Fig. 8 shows the cDNA sequence of the *C. elegans mod-1* gene with the n3034 mutation (SEQ ID NO: 6).

Fig. 9A is a time trace of the MOD-1 channel activated by serotonin.

Fig. 9B is a graph illustrating a dose response curve of MOD-1 channel activity with respect to serotonin concentration.

Fig. 9C is a graph illustrating the peak ionic current conducted by the MOD-1 channel in response to a variety of ligands, including acetylcholine, GABA, glycine, Q-107 (quipazine dimaleate, a 5-HT_3 receptor agonist), and serotonin.

Fig. 10 is a graph illustrating the selectivity the MOD-1 channel has for chloride ions. As the concentration of chloride ions outside of the cell increases, the reversal potential becomes more negative.

Fig. 11 is a time trace of a MOD-1-like response from rat brain RNA.

Fig. 12 is a time trace of a MOD-1-like response of an oocyte injected with rat cortex RNA.

Detailed Description of the Invention

MOD-1 is associated with locomotion in *C. elegans*

Hermaphrodites respond to the presence of a bacterial lawn (their food source) by slowing their rate of locomotion. Animals deprived of bacteria for 30

minutes exhibit enhanced slowing when they encounter a bacterial lawn. Genetic, pharmacological, and laser ablation studies demonstrate that this modulatory response is mediated, in part, by serotonin.

Nematodes to be tested in the locomotion assay were picked as L4 animals 16-20 hours prior to the assay. Locomotion was assayed by placing the nematode on an assay plate (prepared by spreading a solution of *E. coli* strain HB101 on NGM agar in 5 cm plates, using a ring with an inner diameter of approximately 1 cm and an outer diameter of approximately 3.5 cm, and allowing the bacteria to grow 13-15 hours at 37°C), observing each nematode under a dissecting microscope for 20 seconds, and counting the number of dorsal-ventral bends that occur in the anterior portion of the body during the interval.

For satiated animals, locomotion rate was assayed by removing five animals from plates with ample bacteria, washing them in S-basal buffer, and transferring them to the clear zone of the bacterial lawn of an assay plate using a capillary pipette. Beginning five minutes after transfer, the number of body bends was counted, as described above. This procedure was performed for each of the 5 animals.

To assay locomotion rates in food-deprived animals, 5-15 animals were removed from plates with ample food, washed twice in S-basal buffer, and transferred to 5 cm NGM agar plates without bacteria. Food-deprived animals were incubated on these plates for thirty minutes at room temperature, and then were transferred to assay plates. Locomotion was assayed, as described above for satiated animals.

The *mod-1* mutants, obtained from the screen, as described above, exhibited a dominant phenotype of lack of decreased locomotion after being

deprived of bacteria and then returned to a bacterial lawn.

MOD-1 is associated with locomotion seen in *C. elegans* exposed to serotonin

Animals to be tested for sensitivity or insensitivity to serotonin in this liquid locomotion assay were picked as L4 animals 16-20 hours prior to assay and the plates were coded so that the experimenter was blind to the genotype of the animals to be scored. On the day of the assay, serotonin (as a creatinine sulphate salt) was dissolved in M9 (at the required concentrations) just before use, and 200 μl were aliquoted to the wells of a flat-bottomed 96-well polystyrene plate. Twenty nematodes of each genotype to be tested were then transferred from the plate into a well containing liquid, using bacteria as glue. Care was taken not to hurt the animals while dislodging them from the pick, and the animals were observed immediately after transfer to ensure that all of them began to exhibit swimming motions. Then at various time intervals, the number of nematodes in each well that were still actively swimming was quantified.

The *mod-1* mutants, as described in the previous section, were further characterized using this technique. Animals carrying the n3034 mutation exhibited a dominant phenotype of insensitivity to exogenous serotonin in liquid locomotion assays. Animals carrying the ok103 mutation exhibited a recessive phenotype of insensitivity to exogenous serotonin in liquid locomotion assays.

The following examples are provided to illustrate the invention. These examples should not be construed as limiting.

Example 1: Cloning of the *mod-1* gene

Both the wild-type, and mutant *mod-1* cDNAs have been obtained. The

dominant serotonin resistance phenotype of animals carrying the *mod-1(n3034)* allele was used to genetically map *mod-1(n3034)* to a 0.7 map-unit interval on chromosome V. Deficiency analysis showed that the dominant serotonin resistance phenotype is not due to a haploinsufficiency of the *mod-1* locus. The recessive nature of the serotonin resistance phenotype at early time points was exploited to perform standard transformation rescue experiments, and subsequently, the gene was cloned.

Example 2: MOD-1 encodes a ligand-gated ion channel

The protein encoded by the *mod-1* open reading frame responsible for the rescue is structurally similar to ligand-gated ion channels that belong to the nicotinic acetylcholine receptor (nAchR) family. The nAchR family members are all pentameric channels with large N-terminal extracellular ligand-binding domains, four highly conserved transmembrane domains (M1-M4), and relatively divergent cytoplasmic domains between M3 and M4. nAchR family members include channels gated by acetylcholine, glycine, GABA, avermectin, and serotonin. Within the members of the nAchR family, structure-function analysis has been performed primarily on the acetylcholine receptor, but many structural and functional parallels have been seen with the other family members as well. In addition, chimeric channel studies show that there is a great deal of conservation at the functional level, even across the different ligand-gated members of the family. The M2 domains of the various subunits are predicted to line the pore of the channels. Site-directed mutagenesis studies of residues within this domain have demonstrated that ion specificity and modulation of the magnitude and frequency of current flux are determined, at least in part, by the residues that line the pore and

those that are immediately adjacent to the pore on both the extracellular and cytoplasmic sides. Based on primary sequence analysis, MOD-1 appears to be equally divergent from all cloned nAchR family members.

Example 3: *mod-1* forms a serotonin-gated anion channel

MOD-1 was heterologously expressed in *Xenopus* oocytes, injected with 50 nl of *C. elegans* RNA, or MOD-1 was expressed in HEK cells transiently transfected by calcium phosphate precipitation. Forty-eight to 72 hours later, the oocytes or cells were screened under a voltage clamp. Application of 100 nM serotonin elicited large inward currents at a holding potential of -70 mV. Uninjected oocytes and nontransfected cells had no response to 10 μM serotonin. Application of 1 mM of other agonists of ligand-gated ion channels, such as acetylcholine, GABA, or glycine elicited little or no response from the MOD-1 channel.

Pretreatment of wild-type *C. elegans* with mianserin or methiothepin, serotonin receptor antagonists, prevents food-deprived animals from exhibiting the wild-type enhanced slowing response after they encounter bacteria. For this reason, even though both compounds have thus far been considered primarily to be antagonists of metabotropic serotonin receptors, we tested their abilities to affect MOD-1 in oocytes. The MOD-1 channel was inhibited by mianserin and methiothepin, with approximate K_i values of 19 μM and 32 μM, respectively. Pre-treatment of *mod-1* mutants with mianserin or methiothepin did not further affect the defective enhanced slowing response of these animals. These data indicate that mianserin and methiothepin interfere with the enhanced slowing response of *C. elegans* by antagonizing the MOD-1 serotonin-gated chloride channel.

Example 4: MOD-1 is permeable to chloride ions

Ion selectivity was determined by measuring changes in the reversal potential (voltage at which the serotonin response changes from an inward, negative, to an outward, positive, current) in response to varying the ionic composition of the bath solution. The reversal potential was insensitive to changes in cations (Na^+ or K^+), but shifted by approximately 50 mV for each 10-fold change in extracellular chloride concentration.

Example 5: Antibodies to MOD-1

Using MOD-1 polypeptides described herein, anti-MOD-1 antibodies were produced using standard techniques. Peptides to either the putative N-terminal extracellular domain, or to a putative C-terminal intracellular domain, located between transmembrane-spanning regions III and IV, were synthesized, and coupled to GST using standard techniques. The peptides were used to immunize two different rabbits and three different rats. The antibodies were then affinity purified on a HIS-tagged-MOD-1 affinity column using standard techniques, and were shown to specifically identify GST-MOD-1, by Western blot techniques.

Polypeptides for additional antibody production may be produced by recombinant or synthetic peptide techniques (see, e.g., Solid Phase Peptide Synthesis, 2nd ed., 1984 The Pierce Chemical Co., Rockford, IL; Ausubel et al., *supra*).

Alternatively, monoclonal antibodies may be prepared using a serotonin-gated anion channel polypeptide (or immunogenic fragment or analog) and standard hybridoma technology (see, e.g., Kohler et al., Nature 256:495, 1975;

Kohler et al., Eur. J. Immunol. 6:511, 1976; Kohler et al., Eur. J. Immunol. 6:292, 1976; Hammerling et al., In *Monoclonal Antibodies and T Cell Hybridomas*, Elsevier, NY, 1981; Ausubel et al., *supra*).

Once produced, polyclonal or monoclonal antibodies are tested for specific recognition by Western blot or immunoprecipitation analysis (by the methods described in Ausubel et al., *supra*). Antibodies that specifically recognize a serotonin-gated anion channel polypeptide, as described herein, are considered to be useful in the invention. Anti-serotonin-gated anion channel antibodies, as isolated above, may be used, e.g., in an immunoassay to assay or monitor the level of a serotonin-gated anion channel polypeptide produced by *C. elegans* or a mammal, or to screen for compounds that modulate serotonin-gated anion channel polypeptide production. Anti-serotonin-gated anion channel antibodies may also be used to identify cells that express a serotonin-gated anion channel gene.

Example 6: Cloning of mammalian serotonin-gated chloride channels with biophysical properties similar to the *C. elegans* serotonin-gated anion channel

Based on our isolation of a novel nematode *mod-1* cDNA, the isolation of mammalian nucleic acid sequences encoding a serotonin-gated anion channel, including human sequences, is made possible using the strategies described herein and standard techniques.

I. Expression cloning using *Xenopus* oocytes

A. Poly(A)+ RNA isolated from various tissues types is injected into *Xenopus* oocytes. Initial screening is performed on total Poly(A)+ RNA from human brain, human spinal cord, human testes, rat brain, rat testes, mouse brain, and mouse

testes.

B. Functional expression of serotonin-gated ion channels is assayed by measuring ion current in voltage-clamped oocytes elicited by application of serotonin at a concentration of 100 nM or less. Several strategies can be used to identify those serotonin-gated currents that are likely to be conducted by an anion-selective ionotropic channel, comparable to MOD-1.

1) High affinity for serotonin. We have found that MOD-1 channels are activated by lower concentrations of serotonin than 5-HT_{3a} type serotonin receptors. MOD-1 has a half-maximal response with 50 nM serotonin. For 5-HT_{3a} channels, no response is detectable in 1μM serotonin, but 10 μM serotonin elicits a robust current. The lower affinity of the 5-HT_{3a} receptor for serotonin is also reflected in its faster and more complete "washout" (reduction of current back to baseline when the drug is washed off) compared to MOD-1. Serotonin-gated anion channels that have a lower affinity for serotonin can also be isolated using the methods, as described above.

2) Shifts in the reversal potential caused by changes in $[Cl]_o$. In standard external saline (140 mM NaCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, 2.5 mM glucose, and 10 mM HEPES) the reversal potential (E_{rev}) for MOD-1 is about -20 mV, whereas the 5-HT_{3a} current reverses at about 0 mV. Decreasing the extracellular Cl^- to 50 mM by

substitution with gluconate, while keeping the cation concentration fixed, will cause E_{rev} of the MOD-1 current to shift to > +15 mV whereas E_{rev} for the 5-HT_{3a} current will not be changed.

3) Exclusion of metabotropic (second messenger dependent) serotonin-gated currents. Ligand binding to metabotropic 5-HT receptors, such as the 5-HT_{1C} receptor, expressed in *Xenopus* oocytes elicits a large Cl^- current due to IP_3-triggered release of intracellular Ca^{2+} and subsequent activation of endogenous Ca^{2+}-activated Cl^- channels. This signaling pathway can be suppressed by direct injection of IP_3, which exhausts the stores of releasable Ca^{2+} and thereby causes the oocyte to be refractory to metabotropic 5-HT receptor responses that depend on internal Ca^{2+} release. Serotonin-gated responses acting through second messenger systems also differ from ionotropic responses in that second-messenger based systems often give rise to oscillations in ion current. These oscillations arise from the dynamic aspects of intracellular Ca^{2+} regulation. In contrast, current conducted by ionotropic receptors always have a monophasic time course.

4) 5-HT_{3a} specific toxin. The 41-amino acid snail venom σ-conotoxin GVIIIA is a potent competitive antagonist of the 5-HT_{3a} channel (IC 50 on the order of 50 nM). One can test whether MOD-1, like all other known 5-HT class receptors, is insensitive to μM concentrations of this conotoxin. This strategy may provide a simple

method for eliminating the only other known serotonin-gated ionotropic receptors (5-HT_{3a} and 5-HT_{3b}).

5) Suppression of all known forms of serotonin channels. Ideally, expression cloning of mammalian serotonin-gated chloride channels is achieved under conditions in which all other known serotonin gated channels and receptors are blocked. The blockage of these serotonin gated channels and receptors can be accomplished by bathing the oocyte in compounds that inhibit their function. For example, the oocytes may be bathed in a solution containing the calcium chelator BAPTA-AM. The concentration of BAPTA-AM in the bath is approximately 200 μM. While BAPTA-AM blocks other known serotonin gated receptors, it does not affect the function of MOD-1.

Alternatively, the bath may contain a high concentration of calcium, for example, approximately 10 mM, that is sufficient to block serotonin gated cation channels, but does not block MOD-1. In another method, serotonin gated Na^+/K^+ channels may be blocked using, for example, choline chloride or N-methyl glucamine. In other methods, the bath may contain, specific serotonin antagonists. For example, granisetron or ondansetron (at approximately 1 μM concentrations) may be used to inhibit the serotonin-gated cation channel.

One skilled in the art can appreciate that a combination of these methods may provide the maximal blockage of all known serotonin gated ion channels and receptors. For example, one preferred combination of

serotonin gated channel and receptor blockers is BAPTA-AM and/or choline chloride or N-methyl-glucamine.

A method to identify a mammalian serotonin-gated chloride channel was carried out essentially as described above. Oocytes were injected with rat cortex RNA. Six days later, the oocytes were bathed in BAPTA-AM (200 μM) for 2 hours at room temperature, to deplete internal Ca^{++} stores, thereby preventing G-protein-coupled serotonin receptors from having an effect through calcium-dependent second messenger pathways. The oocytes were then screened under a voltage clamp, in a buffer containing 96 mM NaCl, 2 mM KCl, 0.3 mM $CaCl_2$, 1 mM $MgCl_2$, and 5 mM HEPES (pH 7.5), and with 100 mM Tris added. Addition of Tris completely blocks the 5-HT_3 cation channel. Application of 1 μM serotonin for 1 minute elicited inward currents at a holding potential of -70 mV in about 10% of the oocytes (Fig. 11).

These results indicate that rat brain RNA elicits a MOD-1-like serotonin-activated current from oocytes. This current is not a 5-HT_{3a} (and is very unlikely to be another permeant 5-HT ionotropic cation channel receptor) or a G-protein-coupled serotonin receptor-activated current. The isolation of the specific RNA that mediates these results is achieved, as described below.

In additional studies, oocytes were injected with poly(A)+ RNA from rat cortex, striatum, or thalamus, as described above. The oocytes were bathed in 200 μM BAPTA-AM for 2 hours, and were then screened under a voltage clamp, in a bath solution containing 2 mM Co^{2+} to block 5-HT_{3a} responses. Application of 1 μM serotonin elicited inward currents at a holding potential of -70 mV in approximately 33% of the oocytes. Fig. 12 is a representative time trace of a

MOD-1-like response from an oocytes injected with rat cortex RNA. These MOD-1-like currents were not detected in oocytes injected with rat RNA from spinal cord, heart, lung, or testes.

C. When a response that fits some or all of the criteria outlined above has been identified, one can size fractionate the RNA as the first step toward isolating a specific RNA (and corresponding cDNA). Our preliminary studies of MOD-1 and data from the cloning of the 5-HT_{3a} cation channel demonstrate that functional serotonin-gated channels can be formed by homomultimers of a single gene product. This result tremendously improves the feasibility of the expression-cloning strategy. A single RNA species is capable of coding for a functional ionotropic channel, which implies that RNA size fractionation should not cause a loss of serotonin response, as might occur with a heteromultimeric channel protein. Sucrose gradients are used to size fractionate total RNA and individual fractions are injected into oocytes to test for serotonin-gated responses. Once a small enough pool has been determined by such methods, the RNA from that pool is used to prepare cDNA libraries in appropriate vectors. Resulting clones are end-sequenced, and RNA is synthesized from distinct clones and tested in oocytes for the required activity. Clones that produce the desired response are then sequenced in their entirety.

If the results from these experiments indicate that the mammalian serotonin-gated anion channel consists of a heteromultimer rather than a homomultimer, then various pools of mammalian RNA are injected into the oocyte along with any RNAs encoding putative serotonin-gated anion channels. The functional expression of serotonin-gated anion channels can be assayed, as described above.

When a pool meets the requirements of contributing to the make-up of a serotonin-gated anion channel, as outlined above, the pool can be further fractionated, and the assays, as described above, are repeated. The methods used to identify and clone the heteromultimers of the serotonin-gated anion channel then proceed, as described above.

Alternatively, a cDNA library, for example, a human or rat brain cDNA library can be functionally screened to identify and clone mammalian serotonin-gated chloride channels. To this effect, a rat brain cDNA library, containing 10^9 plaque forming units from greater than 10^7 clones with insert sizes of 1.3 to 2.5 kb that have been directionally cloned into the expression vector cmvSPORT, was purchased (Gibco). The library was divided into 20 plates. Colonies were pooled from within one plate, and DNA plasmids were isolated and linearized using restriction enzymes. RNA was then synthesized, using standard methods.

Oocytes are injected with the synthesized RNA (50 - 100 ng) and responses to serotonin, in the presence of BAPTA-AM and 2 mM Co^{2+} are recorded. As a control for the quality of the library and RNA synthesis, serotonin was applied to oocytes not exposed to the BAPTA-AM. Large oscillatory currents were observed. Such responses are typical of metabotropic serotonin receptors, and indicate that the quality of the library and the RNA synthesis is good.

II. Electrophysiological screening of endogenous serotonin-gated currents

If the above expression-cloning strategy is not successful, or in the alternative, one can identify MOD-1 like serotonin-gated responses in mammalian cells. Both acutely dissociated neurons and brain-derived cell lines may be screened. Once a cell type with a robust serotonin-gated, ionotropic, anion-

selective current is identified, these cells are used as an enriched source from which to isolate mRNA coding for a MOD-1-like receptor. Poly(A)+ RNA is then prepared from the positive tissue or cell line, and the same strategy as the one outlined in I is used to identify the clone(s) responsible for the response.

III. Other approaches

In addition to the expression cloning strategies outlined above in sections I and II, complementary approaches can be taken to identify mammalian serotonin-gated chloride channels.

A. EST databases are be systematically combed for sequences with similarities to the *mod-1* cDNA or protein sequence. This process is greatly enhanced by the identification of regions of the MOD-1 protein that allow it to be gated specifically by serotonin, and the regions of the protein that are predicted to be important for allowing anions to pass freely through the channel pore. Existing search algorithms for transmembrane topology (MEMSAT, TMAP, PHDtopology), protein fold motifs (TOPITS, UCLA-DOE Structure Prediction Server), and three-dimensional structures (SCOP) are used to search for sequences that may be clear candidates for mammalian homologs of MOD-1. Full-length cDNAs for such candidates are obtained and tested in the above-described oocyte expression system for the desired response.

B. Hybridization techniques are used to clone additional serotonin-gated anion channels. These techniques are well known to those skilled in the art, and are described, for example, in Ausubel et al., *Current Protocols in Molecular Biology*,

John Wiley & Sons, New York, NY, 1990, and *Guide to Molecular Cloning Techniques*, 1987, S.L. Berger and A.R. Kimmel, eds., Academic Press, New York. If desired, a combination of different oligonucleotide probes may be used for the screening of a recombinant DNA library. The oligonucleotides are, for example, labeled with ^{32}P using methods known in the art, and the detectably-labeled oligonucleotides are used to probe filter replicas from a recombinant DNA library. Recombinant DNA libraries (for example, human cDNA libraries, such as brain or testes-derived cDNA libraries) are prepared according to methods well known in the art, for example, as described in Ausubel et al., *supra*, or are obtained from commercial sources.

For detection or isolation of closely related serotonin-gated anion channel sequences, high stringency hybridization conditions are employed; such conditions include hybridization at about 42°C and about 50% formamide; a first wash at about 65°C, about 2X SSC, and 1% SDS; followed by a second wash at about 65°C and about 0.1% SDS, 1X SSC. Lower stringency conditions for detecting a gene encoding a serotonin-gated anion channel having less sequence identity to the nematode *mod-1* gene described herein include, for example, hybridization at about 42°C in the absence of formamide; a first wash at about 42°C, about 6X SSC, and about 1% SDS; and a second wash at about 50°C, about 6X SSC, and about 1% SDS.

C. Oligonucleotides that partially encode, or are complementary to nucleic acids encoding serotonin-gated anion channel-specific oligonucleotides are used as primers in PCR cloning strategies. Such PCR methods are well known in the art and are described, for example, in *PCR Technology*, H.A. Erlich, ed., Stockton

Press, London, 1989; *PCR Protocols: A Guide to Methods and Applications*, M.A. Innis, D.H. Gelfand, J.J. Sninsky, and T.J. White, eds., Academic Press, Inc., New York, 1990; and Ausubel et al., *supra*. Again, sequences corresponding to sequences thought to encode amino acids important for serotonin-gated anion channel structure or function are preferred for use in isolating other sequences structurally and/or functionally related to a serotonin-gated anion channel. Such sequences are used to screen cDNA, as well as genomic DNA libraries. The sequences also include those that are not known to be important for serotonin-gated anion channel structure or function.

D. Once full-length clones are isolated from the appropriate cDNA library, they are tested in the oocyte, or other suitable cell, for the desired response. The PCR and hybridization cloning strategies, as described above, are enhanced by knowledge of regions of the MOD-1 protein capable of binding serotonin and/or conducting chloride ions. The strategies, however, can be used even without identification of regions of the MOD-1 protein capable of binding serotonin and/or conducting chloride ions.

E. Receptors for small ligands have been found using assays for ligand-binding. Serotonin is immobilized to a solid-support using a linker, and established mammalian cell lines and cells injected with cDNA pools from various tissue sources are assayed for binding to serotonin. Cells that bind are isolated and the cDNA from within the cell is isolated using single-cell PCR. This step can be used as an enrichment step before proceeding with strategies outlined in section I. The cDNA clones are sequenced and those that fit the general protein topology

constraints for ligand-gated ion channels are tested for the serotonin-gated anion channel-like characteristics in the ooctye system, or other suitable systems.

E. An antibody to MOD-1 can also be used to detect cross-reacting mammalian proteins. This can be done by co-immunoprecipitations, using the MOD-1 antibody, and standard techniques.

Example 7: Screening systems for identifying therapeutics

Based on our experimental results, we have developed a number of screening procedures for identifying therapeutic compounds (e.g., pharmaceuticals to treat disorders associated with serotonin-mediated cellular responses), or leads for such compounds, that can be used in human patients. In particular examples, compounds that specifically down-regulate or specifically increase serotonin-gated anion channel biological activity or the biological activity of their human homologs are considered useful in the invention. Also useful in the invention, are compounds that specifically affect other serotonin receptors and a serotonin-gated anion channel, or other serotonin receptors, but specifically not a serotonin-gated anion channel. In general, the screening methods of the invention involve screening any number of compounds for therapeutically active agents by employing any number of *in vitro* or *in vivo* experimental systems. Exemplary methods useful for the identification of such compounds are detailed below.

The methods of the invention simplify the evaluation, identification, and development of active agents for the treatment of conditions associated with serotonin-mediated cellular responses, such as depression, panic disorders, obsessive compulsive disorder, sleep disorders, eating disorders, nausea and

vomiting, other gastrointestinal disorders, and migraines, and the side-effects associated with these drugs. In general, the screening methods provide a facile means for selecting natural or synthetic product extracts or compounds of interest from a large population. These candidates are further evaluated and condensed to a few active and selective materials. Constituents of this pool are then purified and evaluated using methods described herein, to determine their ability to modulate serotonin-mediated responses and conditions.

Below we describe screening methods for evaluating the efficacy of a compound for use in the treatment of diseases associated with serotonin-mediated neurotransmission.

Test extracts and compounds

In general, novel drugs for the treatment of serotonin-mediated cellular responses and conditions are identified from large libraries of both natural product, or synthetic (or semi-synthetic) extracts or chemical libraries according to methods known in the art. Those skilled in the field of drug discovery and development will understand that the precise source of test extracts or compounds is not critical to the screening procedure(s) of the invention. Accordingly, virtually any number of chemical extracts or compounds can be screened using the exemplary methods described herein. Examples of such extracts or compounds include, but are not limited to, plant-, fungal-, prokaryotic- or animal-based extracts, fermentation broths, and synthetic compounds, as well as modifications of existing compounds. Numerous methods are also available for generating random or directed synthesis (e.g., semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, and nucleic acid-based

compounds. Synthetic compound libraries are commercially available from Brandon Associates (Merrimack, NH) and Aldrich Chemical (Milwaukee, WI). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant, and animal extracts are commercially available from a number of sources, including, but not limited to, Biotics (Sussex, UK), Xenova (Slough, UK), Harbor Branch Oceangraphics Institute (Ft. Pierce, FL), and PharmaMar, U.S.A. (Cambridge, MA). In addition, natural and synthetically produced libraries are produced, if desired, according to methods known in the art, e.g., by combinatorial-chemistry methods or standard extraction and fractionation methods. Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

In addition, those skilled in the art of drug discovery and development readily understand that methods for dereplication (e.g., taxonomic dereplication, biological dereplication, and chemical dereplication, or any combination thereof) or the elimination of replicates or repeats of materials already known for their effects on compounds associated with serotonin-mediated cellular responses should be employed whenever possible.

When a crude extract is found to affect serotonin-mediated responses or conditions, further fractionation of the positive lead extract is necessary to isolate chemical constituents responsible for the observed effect. Thus, the goal of the extraction, fractionation, and purification process is the careful characterization and identification of a chemical entity within the crude extract having activities that affect serotonin-mediated cellular responses. The same *in vivo* and *in vitro* assays described herein for the detection of activities in mixtures of compounds can be used to purify the active component and to test derivatives thereof.

Methods of fractionation and purification of such heterogenous extracts are known in the art. If desired, compounds shown to be useful agents for the treatment of pathogenicity are chemically modified according to methods known in the art. Compounds identified as being of therapeutic value are subsequently analyzed using any standard animal model of serotonin-mediated cellular responses known in the art.

There now follow examples of systems useful for evaluating the efficacy of a molecule or compound in treating (or preventing) a condition associated with serotonin-mediated cellular responses, and the side-effects resulting from the treatment of these conditions.

Assays to be used for identifying compounds that affect serotonin-mediated cellular responses include assaying locomotion rates of nematodes exposed to test compounds. It also includes adding a test compound to a cell and assaying serotonin-gated anion channel expression at the nucleic acid level or at the polypeptide level. The changes in serotonin-gated anion channel RNA levels can be monitored by Northern blot analysis, or by highly sensitive quantitative RT-PCR assays. The changes in the levels of serotonin-gated anion channel polypeptide can be monitored through the use of antibodies, including standard Western blot analysis, and immunohistochemistry.

The invention also includes assays that measure ionic current through a channel as a means of identifying a compound that affects serotonin-mediated cellular responses. In the presence of an agonist, the serotonin-gated anion channel is likely to be activated, and this will lead to an increase in the current carried through the channel. This change in current flow can be measured using standard electrophysiological methods. In the presence of an antagonist, the

serotonin-gated anion channel is likely to be refractory to the application of serotonin, and less, or no current will pass through the channel. Such changes can be measured using standard electrophysiological methods.

The invention also includes assays that measure the concentration of serotonin, or a test compound required to activate a serotonin-gated anion channel, as compared to the 5-HT_3 receptor. In both HEK cell and *Xenopus* oocyte expression systems, serotonin-gated currents are detectable at lower concentration of agonist (10-50 nM) for MOD-1 receptors than for 5-HT_3 receptors(>10 μM). This observation provides a tool for exploring the basis of dose-dependent clinical responses. Effects produced by low-dose serotonin or test compounds may be mediated by serotonin-gated anion channels, while effects at 100-fold higher serotonin or test compound concentrations are likely to arise from a combination of serotonin-gated anion channels and 5-HT_3 type receptor activation.

Example 8: Diagnostic probes

cDNA fragments can be used as hybridization probes for allelic markers for haplotype analysis of human disorders or conditions linked to the locus of a serotonin-gated anion channel locus. Such analyses can also be performed using other standard techniques, such as PCR.

Example 9: Pharmacogenetics of responses to therapeutics for serotonin-mediated conditions

A serotonin-gated anion channel can serve as a marker for determining how an individual might respond to a given therapeutic for a serotonin-mediated condition. Genetic analysis of an individual's serotonin-gated anion channel locus

can be completed as described above. Once a group of major mutant alleles has been established, PCR based genotyping assays can be developed to make a molecular diagnosis of an abnormal serotonin-gated anion channel. When information regarding how individuals with a specific serotonin-gated anion channel allele respond to particular therapies is combined with molecular diagnosis techniques, it is feasible to select an optimal therapy to treat serotonin-mediated conditions.

Example 10: Therapies that modulate conditions mediated by serotonergic pathways: Effect of serotonin-gated anion channel genotype

Patients experiencing a specific condition, or set of conditions, mediated by serotonin are placed into one of four treatment groups: placebo or 3 increasing doses of a given drug. During and at the end of the treatment period, the patients are evaluated for the effect of the drug on modulation of the condition(s). The patients are also evaluated for side-effects experienced as a result of drug administration. Patients are also characterized for the presence of various alleles of a serotonin-gated anion channel, and optionally, other serotonin-mediated receptor alleles and/or their respective protein levels. Results of these studies can be correlated to design therapies that provide optimal relief from the serotonin-mediated condition(s), with the fewest side-effects, in a patient with a specific serotonin-gated anion channel allele, or particular protein levels. In addition, other known serotonin-mediated receptors may be characterized and included in the development of the therapeutic protocol.

The patients can also be genotyped for polymorphisms in specific enzymes required for the metabolism of a given therapeutic used in the treatment of

serotonin-mediated conditions. Such enzymes to be assessed include thiopurine S-methyltransferase (TPMT), dihydropyrimidine dehydrogenase (DPD), aldehyde dehydrogenase (ALDH), glutathione S-transferase (GST), uridine diphosphate glucuronosyl-transferase (UGTs), and cytochrome P450 enzymes. Once knowledge of an individual's drug metabolism profile is obtained, therapies to treat serotonin-mediated conditions can be more optimally designed to provide maximal efficacy with minimal side-effects.

Antisense RNA

1. Design of antisense systems. One way in which antisense RNA can be synthesized is through a system. One example of a system includes, but is not limited to a complete panel of adenovirus constructs. The panel may consist of approximately four types of recombinant virus: A) A sense orientation virus for each serotonin-gated anion channel open reading frame; these viruses are designed to massively overexpress the recombinant protein in infected cells. B) Antisense orientation viruses in which the viral promoter drives the synthesis of an mRNA of opposite polarity to the serotonin-gated anion channel RNA, thereby shutting off host cell synthesis of the targeted protein coding region. C) Sub-domain expression viruses; these constructs express only a partial serotonin-gated anion channel protein in infected cells. D) Control viruses; functional analysis of serotonin-gated anion channel requires suitable positive and negative controls for comparison.

2. Confirmation of recombinant adenovirus function. Verification of the sense adenovirus function involves infection of tissue culture cells and determination of protein expression levels. This can be done by Western blot analysis. Functional

analysis of the antisense viruses may be done at the RNA level using either Northern blots of total RNA harvested from infected tissue culture cells or ribonuclease protection assays. Western blot analysis of infected cells may be used to determine whether the expressed antisense RNA interferes with serotonin-gated anion channel expression in the host cell.

3. Documentation that serotonin-gated anion channel over-expression results in increased serotonin-gated anion channel activity. Determination of whether serotonin-gated anion channel over-expression results in increased serotonin-gated channel activity can be done by measuring the ionic current across a membrane elicited by serotonin using standard voltage-clamping techniques. The surface area of the membrane to be analyzed is pre-determined and remains constant for assaying both over-expressing and control samples.

4. Documentation that antisense serotonin-gated anion channel over-expression results in decreased serotonin-gated anion channel activity. Having confirmed that serotonin-gated anion channel over-expression renders cells more likely to exhibit increased serotonin-gated anion channel activity, one may examine whether the antisense adenoviruses render the same cells resistant to the channel activity, using the above-described methods.

5. Identification of antisense oligonucleotides. Concomitant to the adenovirus work, a series of antisense oligonucleotides to various regions of a serotonin-gated anion channel can also be designed. A generally-accepted model of how antisense oligonucleotides function proposes that the formation of RNA/DNA duplexes in the

nucleus activates cellular RNase H enzymes which enzymatically degrade the mRNA component of the hybrid. Virtually any region of the mRNA can be targeted, and therefore choosing an appropriate sequence to target is somewhat empirical. One site frequently targeted is the translation initiation site. Alternatively, one can design antisense oligonucleotides that systematically "walk" down a nucleic acid sequence of interest. Many factors, including secondary structure of the target mRNA and the binding affinity of the targeted sequence determine whether a particular oligonucleotide will be effective, necessitating several oligos for a serotonin-gated anion channel. Oligonucleotides to serotonin-gated anion channel mRNA can be made based on the available computer algorithms for predicting binding affinities and mRNA secondary structures. These and other oligonucleotides may be tested for their ability to target their respective mRNAs for degradation using Northern blot analysis.

6. *Optimization of oligonucleotides*. A secondary round of oligonucleotides may be made when effective target regions have been identified. These oligonucleotides target sequences in the immediate vicinity of the most active antisense oligonucleotides identified using methods such as those provided above. A second round of testing by Northern blot analysis may be required.

7. *Testing antisense oligonucleotides in vitro*. Following successful identification and optimization of targeting oligonucleotides, one may test these antisense oligonucleotides in tissue culture cells. Experimental procedures may parallel those used in the recombinant antisense adenovirus work. Negative control oligonucleotides with mismatch sequences are used to establish baseline or non-

specific effects. Assisted transfection of the oligonucleotides using, for example, cation lipid carriers may be compared to unassisted transfection. Confirmation of the effectiveness of specific antisense oligonucleotides prompts synthesis of oligonucleotides with modified phosphodiester linkages, such as phosphorothioate or methylimino substituted oligos. These modified oligonucleotides may also be tested *in vitro*.

Another therapeutic approach within this invention involves administration of recombinant protein fragments or antibodies to a serotonin-gated anion channel, either directly to the site where modulation of serotonin transmission is desirable (for example, by injection) or by systemic administration (for example, by any conventional recombinant protein administration technique).

The dosage of serotonin-gated anion channel, the serotonin-gated anion channel fragment, serotonin-gated anion channel mutant protein, or antibody to a serotonin-gated anion channel depends on a number of factors, including the size and health of the individual patient, but, generally, between 0.1 mg and 100 mg inclusive are administered per day to an adult in any pharmaceutically acceptable formulation.

Administration

A serotonin-gated anion channel mutant protein or protein fragment, gene encoding the same, gene encoding a serotonin-gated anion channel antisense RNA, or modulator of a serotonin-gated anion channel may be administered within a pharmaceutically-acceptable diluent, carrier, or excipient, in unit dosage form. Conventional pharmaceutical practice may be employed to provide suitable formulations or compositions to administer the compounds to patients suffering

from a disease or condition associated with the serotonergic pathway. Administration may begin before the patient is symptomatic. Any appropriate route of administration may be employed, for example, administration may be parenteral, intravenous, intraarterial, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, suppository, or oral administration. For example, therapeutic formulations may be in the form of liquid solutions or suspensions; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols.

Methods well known in the art for making formulations are found, for example, in "Remington's Pharmaceutical Sciences," (Remington: The Science and Practice of Pharmacy, 19th ed., A.R. Gennaro, ed., Mack Publishing Co., Easton, PA, 1995). Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for serotonin-gated anion channel modulatory compounds include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or may be oily solutions for administration in the form of nasal drops, or as a gel.

If desired, treatment with serotonin-gated anion channel mutant proteins or serotonin-gated anion channel fragments, related genes, or other modulatory compounds may be combined with more traditional therapies for therapies associated with serotonin-mediated cellular responses.

Example 11: Transgenic mice

Transgenic mouse expression vectors, including neuronal, testes, and smooth muscle cell-specific promoter constructs can be constructed. Founder mice that are viable for most of these constructs can be identified, and breeding colonies can be developed. These mice will likely be prone to modulation of the serotonin-gated anion channel within tissue types in which the promoter is active. Thus the mice provide an excellent resource for testing the efficacy of antisense oligonucleotides, and for screening for therapeutics associated with serotonin-mediated cellular responses and the side-effects associated with these therapeutics. Standard mouse drug screening models and gene delivery protocols may be employed to utilize the mice for this purpose.

Example 12: Characterization of *mod-1* mutants

A single base transition mutation in the *mod-1* coding sequence in *n3034* mutants was found. This missense mutation is predicted to change alanine 281 (codon GCT) to a valine (codon GTT) within the predicted M2 transmembrane domain of the MOD-1 protein (a domain thought to be critical for channel function). Site-directed mutagenesis was used to introduce this C-to-T (A281V) mutation into a 5.5 kb minimal fragment that rescues the mutant phenotype of serotonin resistance, and transgenic animals carrying extrachromasomal arrays of the fragment,

Ex[MOD-1(A281V)], were generated. These transgenic animals displayed resistance to exogenous serotonin, confirming that the C-to-T (A281V) change in the *mod-1* locus was sufficient to cause serotonin resistance.

The effect on channel function of the MOD-1(A281V) substitution in the *mod-1(n3034)* mutant was also examined. When cRNA encoding MOD-1(A281V) was injected into oocytes, there were no serotonin-gated responses. When the mutant cRNA was co-injected with approximately a four-fold excess of wild-type *mod-1* cRNA, the magnitude of the current through the wild-type channels was dramatically reduced compared to oocytes that had been injected in parallel with the same amount of only the wild-type cRNA. These findings indicate that the MOD-1 channel is multimeric and that mutant MOD-1(A281V) channel subunits interfere in a dominant manner with the function of wild-type MOD-1 channel subunits.

To determine the phenotypic consequence of completely eliminating *mod-1* function the deletion allele of *mod-1*, *(ok103)*, was analyzed. This mutant was obtained by screening libraries of mutagenized animals using PCR to identify large deletions in the *mod-1* genomic locus. *mod-1(ok103)* mutants, when food deprived, were defective in the enhanced slowing response, but was not defective in the basal slowing response displayed by well-fed wild-type animals. The deletion mutant was also resistant to exogenous serotonin. The serotonin resistance caused by the deletion allele was completely recessive throughout the 20 minute time course of serotonin exposure, which is consistent with our observation that animals heterozygous for large chromosomal deficiencies that uncover the *mod-1* genomic locus are not serotonin resistant. The molecular nature of the *mod-1(ok103)* mutation suggests that it is a null allele. That null alleles confer the same phenotype as that conferred by the Ex[MOD-1(A281V)] extrachromosomal array suggests that

mod-1(n3034) is a dominant negative allele.

What is claimed is:

1. A substantially pure nucleic acid sequence encoding a serotonin-gated anion channel.

2. A substantially pure polypeptide, said polypeptide being a serotonin-gated anion channel.

3. The nucleic acid sequence of claim 1, wherein said serotonin-gated anion channel is a chloride channel.

4. The polypeptide sequence of claim 2, wherein said serotonin-gated anion channel is a chloride channel.

5. The nucleic acid sequence of claim 1, wherein said serotonin-gated anion channel is MOD-1.

6. The polypeptide sequence of claim 2, wherein said serotonin-gated anion channel is MOD-1.

7. An antibody that specifically binds to a serotonin-gated anion channel.

8. A *Caenorhabditis elegans* (*C. elegans*) strain having a mutant *mod-1* gene.

9. A method for identifying a compound that modulates the biological activity of a serotonin-gated anion channel, said method comprising the steps of:

(a) administering a test compound to a serotonin-gated anion channel; and

(b) assaying a modulation in the biological activity of said serotonin-gated anion channel.

10. A diagnostic probe for detecting conditions associated with a serotonin-mediated cellular response, said probe comprising a means for measurement of a serotonin-gated anion channel.

11. A method for characterizing a drug associated with a serotonin-mediated cellular response, said method comprising detecting a modulation in the activity of a serotonin-gated anion channel when said channel is exposed to said drug.

12. A method for decreasing serotonin-gated anion channel function, said method comprising administering an antisense RNA that decreases the level of a serotonin-gated anion channel polypeptide.

13. A method for decreasing serotonin-gated anion channel function, said method comprising administering an antibody that binds to a serotonin-gated anion channel polypeptide.

14. A method for modulating serotonin-gated anion channel function, said method comprising administering a nucleic acid vector encoding a serotonin-gated anion channel, said administering being sufficient to modulate serotonin-gated anion channel activity.

15. A method for identifying a gene that is structurally related to a gene encoding a serotonin-gated anion channel, said method comprising identifying a gene with a probe derived from said serotonin-gated anion channel gene or a product encoded by said serotonin-gated anion channel gene.

16. An isolated gene identified by the method of claim 85.

17. A transgenic animal that over-expresses a serotonin-gated anion channel.

18. A transgenic animal that under-expresses a serotonin-gated anion channel.

19. A transgenic animal that expresses a dominant negative serotonin-gated anion channel.

20. A method for identifying a compound that modulates the activity of a serotonin-gated anion channel, said method comprising the steps of:

(a) exposing a nematode to a test compound;

(b) assaying the locomotion rate of said nematode; and

(c) comparing said locomotion rate to that of a control nematode receiving no test compound, wherein a modulation in said locomotion rate indicates a compound that modulates the activity of a serotonin-gated anion channel.

21. A method for identifying a compound that modulates the activity of a serotonin-gated anion channel in a liquid locomotion assay, said method comprising the steps of:

(a) exposing a nematode to a test compound;

(b) quantifying the number of nematodes actively swimming after exposure to said test compound; and

(c) comparing the number of said actively swimming nematodes to that of control nematodes receiving no test compound, wherein a modulation in said number of actively swimming nematodes indicates a compound that modulates the activity of a serotonin-gated anion channel.

A Novel Serotonin-Gated Ion Channel

Abstract of the Disclosure

Disclosed is a novel serotonin-gated anion channel that is permeable to chloride ions. Also disclosed are methods for the screening of therapeutics useful for treating serotonin-mediated cellular responses and conditions, as well as diagnostic methods for identifying such conditions.

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        10         20         30         40         50         60
TCATGTTTCA CGGAACGACG AATTTATCCC GTCGTTTCTT CCTTTCCGTT TTAACTCATA

        70         80         90        100        110        120
TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTT GTTTTTTCGT

       130        140        150        160        170        180
CGTTTAATTG TGGAAACACA TATCCGTCCT CTTTGAAACA GCATCAGAAA ACTTTCTGCT

       190        200        210        220        230        240
CTCCGTGTCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACAACTAA

       250        260        270        280        290        300
CTGCCAATGG GAGGAGCCAG TTGGAGCAGG GTGCGTGCTC GGTGCTCTTT TCAGAAGGTT

       310        320        330        340        350        360
TTCTCTTGTG CCAGCATGCT TTTTTGAGGC TGTGTCATCA CAATGAACAT GTGTGAGTTC

       370        380        390        400        410        420
ATCCGTCTGG ATTATTCTTT TTCTTACGTC TTCTGAGTAC TTCATACTTT CCAAATTTTT

       430        440        450        460        470        480
CAACTGAACT TTTCTTCTTT TCTCATTGAA GTGGTTTGGT TTTGGTCGCG TGATCAACGG

       490        500        510        520        530        540
ATCCTACTTT TTTGAAACAA AATGTTTTTG AAGTTTCACA GACTGATTTC GGGGTTTTTT

       550        560        570        580        590        600
CAAAGAATAT ATTCCCTCTC GAGCAAGAGA AAATTCCAGA AAATAGTAGT TTTTTTCAAT

       610        620        630        640        650        660
TAGTCGTTTC ATTTGTACTA GCTAAAAAAC TTGCAACTTA TGGCTTTAAA ACATGTGTTG

       670        680        690        700        710        720
GCTTCATACA AAAACATTTA ACTAGTGTTT TTCCAGTTTT GTGTTCGTTT CATTTTCTCA

       730        740        750        760        770        780
CCAAACTGAC AATAATTACT TTCTGTGAAC GTGTTTTGTA GGCAAGCTCC CGAATATTTT

       790        800        810        820        830        840
TTTCTCTTCT CACGTCTTGT TATTTTCTCG ATTTTATTTT CTGAATCTGT GCGGTTTTCA

       850        860        870        880        890        900
ATCAATTTGA TTGCGATAAT TATTCTATCA GAAATATATT TTCAGAAATC CAAATACTCC

       910        920        930        940        950        960
AGGTGCCAAT GCGGTGAAAG AAAATTATGA AGTTTATTCC TGAAATCACA CTACTCTTGC

       970        980        990       1000       1010       1020
TTTTATTTGT ACACTCTACA CAGGTTAGTT GGTTGATTCT AGATCTCTTG CCTCCTAGCT

      1030       1040       1050       1060       1070       1080
TGCAAGGATA ATATAATTGA ATTGTTTTTG AGGAGTGCAA AGATTGAATA GTTTTCTATA

      1090       1100       1110       1120       1130       1140
TTTAGGCTAA AGGAAAACGA CGGAAATGTC CGGAGGGTGC GTGGTCGGAA GGAAAGATTA
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Fig. 1
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      1150       1160       1170       1180       1190       1200
TGAACACGAT CATGAGCAAC TACACGAAAA TGTTGCCCGA CGCGGAGGAC AGCGTACAAG

      1210       1220       1230       1240       1250       1260
TTAATATTGA GATTCATGTA CAGGTTGGTA GACTCTATAA TTGCACACCA ATATGTGAAA

      1270       1280       1290       1300       1310       1320
GTTTTCTTTA AAATTAAACT GCTGTAAATG ACTTTTGAAT AAGTTTATCA GATAGAAATT

      1330       1340       1350       1360       1370       1380
GTCTGAACTT TTCGATTCAA ACTTTCCGAA CTTCAAAGCG GTTCCAAATT ACTCACTTCC

      1390       1400       1410       1420       1430       1440
ATTTATCTCT TTGCTACAAT TTCTCCCACA AAGCCTTTTT CTTCATTTAA CGTTCTTTTT

      1450       1460       1470       1480       1490       1500
TATGTCGTTG TTCTTACAAA CAATTTCGTC TCCTTGATGA ACTGCTTGAA CTGAGAATAG

      1510       1520       1530       1540       1550       1560
TCACATGAGG ATAAATTTGA TGGAATGACA AGTTTTGTGC CCAGAAGGCA GTTTTGCACT

      1570       1580       1590       1600       1610       1620
GAACTTGTTC AGTTGCAGAC ACATCTCAAA ACACAGAAGA TGAGTGGAAA ACTAGTGAGA

      1630       1640       1650       1660       1670       1680
GACTGCCAAA AGTCGAAGGG ATAATGAAAA TTTGTTGCAA ATGAATTCTG CGAAGTTATG

      1690       1700       1710       1720       1730       1740
TGAAAAATTA TTGGATTGGG AGTTGTGGGA GTGAAGAGAT GGGTCAAAAG CCATCAATCT

      1750       1760       1770       1780       1790       1800
TGAATGCTTC GGTCAAAGAT TTGTTTCTCA TATGTTTACA ACACTGAAAA CAATCTATCC

      1810       1820       1830       1840       1850       1860
TAGAAATGTT TGAACCACCC TCTAAAGTCC TTCCGTATAT TTTTTCATCT TTATACCGAC

      1870       1880       1890       1900       1910       1920
CAGAATTCAA GAGTTGTTTG AAATAACTTC CTCTTTTTTG GAGAATATGT ACTCAGATTT

      1930       1940       1950       1960       1970       1980
TTACATTCAA AATTTATATA TTTTCAAATA GAAAAAGTGC CAAGTACCAG AAACTTTTAT

      1990       2000       2010       2020       2030       2040
CAAGTTGGCG GCACTTTGGA GAGTGAATTT GATGAAAAAG TGTTTGATAA GTTTGTCGGG

      2050       2060       2070       2080       2090       2100
CAAACTGGTC CCCTGGGTGG GGAAATGGTG GCATTTTTGG AAACATTTTC ATAGTCGAAG

      2110       2120       2130       2140       2150       2160
AAGTGGAACA AGAAAATTGG AAAATAGAGA TACATATGTA TATGAAAATA GAATTGAACA

      2170       2180       2190       2200       2210       2220
GGAACTTATT TTTATTTTCA GGATATGGGA AGCTTGAATG AAATATCATC CGACTTTGAA

      2230       2240       2250       2260       2270       2280
ATTGACATTT TATTCACTCA ACTGTGGCAT GACTCGGCAC TTTCTTTTGC TCATCTTCCG
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Fig. 1

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      2290        2300        2310        2320        2330        2340
GCTTGTAAGC GGTAAGAAAT CTTTGTATTA GAAGGGAAAA ATATTTAAAT TAATGAAATT

      2350        2360        2370        2380        2390        2400
TCAGAAATAT CACAATGGAA ACACGACTTT TACCTAAGAT TTGGTCTCCA AACACGTGTA

      2410        2420        2430        2440        2450        2460
TGATTAATTC AAAACGAACA ACCGTCCATG CATCACCATC GGAAAATGTG ATGGTTATTC

      2470        2480        2490        2500        2510        2520
TGTACGAGGT ATGATTTTTG ATTTTGTGAC GTCACAAACA GAGCATGTCT AAGGGCATGT

      2530        2540        2550        2560        2570        2580
TGTAGCAAGA AAAAAACGGA TTCTTGTCTC TGTCGACGTT TCCTAAGTAT TGTGAATTAT

      2590        2600        2610        2620        2630        2640
TTATAATACA TCACTCTAAT TACGTGAATA CTTACACGTT TAACTGGGTG AAGGATAAAA

      2650        2660        2670        2680        2690        2700
TAGAGAAGGA GACGTTGAAA AAGCTCTTCG GTAGATTAAA GAGTCTAGAA TCGACATATG

      2710        2720        2730        2740        2750        2760
TATTCATGTT TCTCGGTTCA GGGAAATAAG TGATTTTGGC GAAAAAGAGT TAGACGACAT

      2770        2780        2790        2800        2810        2820
TTTTTAGAAA ACTAAAACTA TATTCTCGAA CCCAAATCAG TCTAATGGTT TTCAGCAAAA

      2830        2840        2850        2860        2870        2880
AGTATGAAAT ATACAATGTT TGTTTCAGAA TACCCAGTAC AAAATTTGAA GTTTTTCAGA

      2890        2900        2910        2920        2930        2940
ATGGAACAGT CTGGATTAAC CATCGTCTTA GTGTCAAATC ACCTTGCAAT TTGGATCTGC

      2950        2960        2970        2980        2990        3000
GACAGTTTCC TTTCGATACT CAAACTTGCA TATTAATCTT TGAATCCTAT AGTCATAACT

      3010        3020        3030        3040        3050        3060
CAGAAGAAGT TGAACTTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG CCAATTCAAC

      3070        3080        3090        3100        3110        3120
TTCCTGACTT TGATATGGTT CATTATTCAA CTAAAAAGGA AACTTTACTC TATCCAAACG

      3130        3140        3150        3160        3170        3180
GGTACTGGGA TCAGCTTCAA GTTACTTTCA CTTTCAAACG ACGATATGGA TTCTATATTA

      3190        3200        3210        3220        3230        3240
TTCAAGCCTA TGTTCCAACA TATCTTACAA TCATTGTATC TTGGGTTTCA TTCTGCATGG

      3250        3260        3270        3280        3290        3300
AACCAAAAGC TCTGCCGGCA AGAACAACTG TCGGAATCTC ATCTCTTCTA GCTCTTACTT

      3310        3320        3330        3340        3350        3360
TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA GGTTTGTTTT

      3370        3380        3390        3400        3410        3420
TTTTCTTTTT CAAACAAATA AAAAAAAAGA TAAACAAATA TTTGTTTCAG CAATGGATGT
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Fig. 1
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      3430        3440        3450        3460        3470        3480
GTGGATGCTT GGATGCATAT CATTTGTCTT CGGAACCATG GTAGAATTGG CATTTGTTTG

      3490        3500        3510        3520        3530        3540
TTACATTTCC CGTTGTCAGA ACAGCGTAAG AAAGTGAGTT GGCATAAGAG TTTTCTCACG

      3550        3560        3570        3580        3590        3600
TGGAGGGAAG TAATTAAATT TTGGGTGTCA TATGAAAATA TCAAAAACAA TATCAGGAAA

      3610        3620        3630        3640        3650        3660
TTGAATTTCA CTATGATTTC GTAGTAAACA AATTACAGCG CGGAACGACG ACGGGAACGA

      3670        3680        3690        3700        3710        3720
ATGAGAAATT CTCAGGTGTG GGCAAACGGA TCGTGTAGAA CTAGAAGCAA CGGGTATGCA

      3730        3740        3750        3760        3770        3780
AACGGGGGAT CTGTAATCTC ACATTATCAT CCAACAAGCA ATGGAAATGG GAATAATAAT

      3790        3800        3810        3820        3830        3840
CGACATGATA CACCTCAAGT TACTGGAAGG TTAGCAATCT CTATGATAGC ATTTATCAAT

      3850        3860        3870        3880        3890        3900
TATTAAAGAA CTCTGGAATT AGTTTTTAAA GTATAAATAA ATCTCTATTT CTTGCGACCT

      3910        3920        3930        3940        3950        3960
ACATTGAACT TAATAGTTAT GTTTTACAGA GGATCACTTC ATCGAAACGG GCCACCATCT

      3970        3980        3990        4000        4010        4020
CCATTAAACC TTCAAATGAC TACATTTGAT TCGGAGATCC CTCTGACTTT TGATCAGGTG

      4030        4040        4050        4060        4070        4080
AGTCTTACAT TGAGTTCAAA CTTTTTGAAT TTAAGCGTTC TATCTGATAA AGTTCTTCGG

      4090        4100        4110        4120        4130        4140
TGGTTTTATA ATTTTTGATT CATAAACTTA CCCACTCCTT TCTCACTAAC ATTTTACCCT

      4150        4160        4170        4180        4190        4200
GTTCAGCTGC CAGTTTCCAT GGAATCCGAT AGACCCCTGA TTGAAGAGGT AACTGTGAAA

      4210        4220        4230        4240        4250        4260
GTAGTCAATT AATTCCCTGT GTTTCTACCC CACTCAATCC TTTTGTATTT TTTGTTCAGT

      4270        4280        4290        4300        4310        4320
CTATCCACTA TCAATGTCTT ATCACCTCTA GATACTGTTT AGAAGAAAAT ATTGTTCACA

      4330        4340        4350        4360        4370        4380
GTTATGGAAA TCACATATAC TTTGTTCTGG AATTGTATAT GTATGCTTTG AAAAAGCACA

      4390        4400        4410        4420        4430        4440
TTAGAATACT ACAAACATTA GTTTCCATCA GATTTTTGAT TTATCAAAAC CGTTATATTA

      4450        4460        4470        4480        4490        4500
GACACTCTTA AGTTATCATA TTCTAATTTC CAAGAATGTT ATATTTTGAA GAAGCCGGTG

      4510        4520        4530        4540        4550        4560
ATTGTCAAAA AGATTGAAAA CTCCGAGTTT CTATATATGC GAAATTTTCA CTTCAGCCCA
```

Fig. 1
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4570 4580 4590 4600 4610 4620
CACACACACA CACACATTCA CGAAACTTTG TGTTGTTTAT GTTACTTATA TGTTATCTTT

4630 4640 4650 4660 4670 4680
TCTGTCTGAT CATGGTTTTC GGACTGAAAT TGTGTTAATC GGAAGTTATA TGTGAGCCAC

4690 4700 4710 4720 4730 4740
ATTGATTAAA CCTGTGAGAG ATGCCCATTT GTACTCATTT TACGACTGTC TCATGTCCAA

4750 4760 4770 4780 4790 4800
ACACCATGTT TATTGTAATT ACCAGGCTAC TATTTGCAGA TGCGATCAAC ATCACCACCT

4810 4820 4830 4840 4850 4860
CCACCATCTG GATGTCTGGC CAGATTCCAT CCGGAAGCAG TGGACAAATT CTCCATTGTA

4870 4880 4890 4900 4910 4920
GCTTTTCCAT TGGCATTTAC AATGTTTAAT GTTAGTTAAT CCACAGTTAA AAATTCCCAT

4930 4940 4950 4960 4970 4980
AATCATAAAT ATCTCGACTT TTCAGCTTGT CTACTGGTGG CACTATTTGT CTCAAACTTT

4990 5000 5010 5020 5030 5040
CGATCAAAAC TATCAGTGAT TGAAGTTTAT CCCTTTTAAT TCCAATAATT CACAGTTGCC

5050 5060 5070 5080 5090 5100
GGTATCTACC TCCATTCTTT TCCGATGATT CGCAGTTTTT CACAGGGTTC AAATGTATCT

5110 5120 5130 5140 5150 5160
CGTTCAATCT TTTTATGGTT ATTTCTCTTG AATGTCCATT TTAATATTTA TAGAACACTT

5170 5180 5190 5200 5210 5220
TTATGTACAT TGTGTTGGTA TTCAATTCGA AAAACAATGA AATTTATTTC TAAATAACTG

5230 5240 5250 5260 5270 5280
CGTTTCTGGG GTTTCTATCA GCACTTACTA GCTGACAAAA ACTTTTCCGT ATTCGGAATT

5290 5300 5310 5320 5330 5340
AGATTTTTAT GCAAGCAATG TTTCATTTTT ACACAGTATA GTATTTATTC TTACTTTTGA

5350 5360 5370 5380 5390 5400
TTATATTGCT CGCACCCTAA ATGACAGGTA TTAGAAATTA ACCGCTTTTC AGAGTATTTT

5410 5420 5430 5440 5450 5460
TAATCTTCTT AGTACTAGTT TAGTTCTTTA AATAAGAAAC CATCTAGTTT TTCATTATCA

5470 5480 5490 5500 5510 5520
CTCAACTTCA GTCGGACAAA TTTTAAATTT TTTACTCGAT AAAAAAATTT TATAATTCAG

5530 5540 5550
ACAAATTATG TCTTCTCATT TTTGATCGCT

Fig. 1

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        10         20         30         40         50
ATGAAGTTTA TTCCTGAAAT CACACTACTC TTGCTTTTAT TTGTACACTC

        60         70         80         90        100
TACACAGGCT AAAGGAAAAC GACGGAAATG TCCGGAGGGT GCGTGGTCGG

       110        120        130        140        150
AAGGAAAGAT TATGAACACG ATCATGAGCA ACTACACGAA AATGTTGCCC

       160        170        180        190        200
GACGCGGAGG ACAGCGTACA AGTTAATATT GAGATTCATG TACAGGATAT

       210        220        230        240        250
GGGAAGCTTG AATGAAATAT CATCCGACTT TGAAATTGAC ATTTTATTCA

       260        270        280        290        300
CTCAACTGTG GCATGACTCG GCACTTTCTT TTGCTCATCT TCCGGCTTGT

       310        320        330        340        350
AAGCGAAATA TCACAATGGA AACACGACTT TTACCTAAGA TTTGGTCTCC

       360        370        380        390        400
AAACACGTGT ATGATTAATT CAAAACGAAC AACCGTCCAT GCATCACCAT

       410        420        430        440        450
CGGAAAATGT GATGGTTATT CTGTACGAGA ATGGAACAGT CTGGATTAAC

       460        470        480        490        500
CATCGTCTTA GTGTCAAATC ACCTTGCAAT TTGGATCTGC GACAGTTTCC

       510        520        530        540        550
TTTCGATACT CAAACTTGCA TATTAATCTT TGAATCCTAT AGTCATAACT

       560        570        580        590        600
CAGAAGAAGT TGAACTTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG

       610        620        630        640        650
CCAATTCAAC TTCCTGACTT TGATATGGTT CATTATTCAA CTAAAAAGGA

       660        670        680        690        700
AACTTTACTC TATCCAAACG GGTACTGGGA TCAGCTTCAA GTTACTTTCA

       710        720        730        740        750
CTTTCAAACG ACGATATGGA TTCTATATTA TTCAAGCCTA TGTTCCAACA

       760        770        780        790        800
TATCTTACAA TCATTGTATC TTGGGTTTCA TTCTGCATGG AACCAAAAGC

       810        820        830        840        850
TCTGCCGGCA AGAACAACTG TCGGAATCTC ATCTCTTCTA GCTCTTACTT

       860        870        880        890        900
TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA

       910        920        930        940        950
GCAATGGATG TGTGGATGCT TGGATGCATA TCATTTGTCT TCGGAACCAT
```

Fig. 2
Page 1

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       960        970        980        990       1000
GGTAGAATTG GCATTTGTTT GTTACATTTC CCGTTGTCAG AACAGCGTAA

      1010       1020       1030       1040       1050
GAAACGCGGA ACGACGACGG GAACGAATGA GAAATTCTCA GGTGTGGGCA

      1060       1070       1080       1090       1100
AACGGATCGT GTAGAACTAG AAGCAACGGG TATGCAAACG GGGGATCTGT

      1110       1120       1130       1140       1150
AATCTCACAT TATCATCCAA CAAGCAATGG AAATGGGAAT AATAATCGAC

      1160       1170       1180       1190       1200
ATGATACACC TCAAGTTACT GGAAGAGGAT CACTTCATCG AAACGGGCCA

      1210       1220       1230       1240       1250
CCATCTCCAT TAAACCTTCA AATGACTACA TTTGATTCGG AGATCCCTCT

      1260       1270       1280       1290       1300
GACTTTTGAT CAGCTGCCAG TTTCCATGGA ATCCGATAGA CCCCTGATTG

      1310       1320       1330       1340       1350
AAGAGATGCG ATCAACATCA CCACCTCCAC CATCTGGATG TCTGGCCAGA

      1360       1370       1380       1390       1400
TTCCATCCGG AAGCAGTGGA CAAATTCTCC ATTGTAGCTT TTCCATTGGC

      1410       1420       1430       1440       1450
ATTTACAATG TTTAATCTTG TCTACTGGTG GCACTATTTG TCTCAAACTT

      1460       1470
TCGATCAAAA CTATCAGTGA
```

Fig. 2
Page 2

10 20 30 40 50
MKFIPEITLL LLLFVHSTQA KGKRRKCPEG AWSEGKIMNT IMSNYTKMLP

60 70 80 90 100
DAEDSVQVNI EIHVQDMGSL NEISSDFEID ILFTQLWHDS ALSFAHLPAC

110 120 130 140 150
KRNITMETRL LPKIWSPNTC MINSKRTTVH ASPSENVMVI LYENGTVWIN

160 170 180 190 200
HRLSVKSPCN LDLRQFPFDT QTCILIFESY SHNSEEVELH WMEEAVTLMK

210 220 230 240 250
PIQLPDFDMV HYSTKKETLL YPNGYWDQLQ VTFTFKRRYG FYIIQAYVPT

260 270 280 290 300
YLTIIVSWVS FCMEPKALPA RTTVGISSLL ALTFQFGNIL KNLPRVSYVK

310 320 330 340 350
AMDVWMLGCI SFVFGTMVEL AFVCYISRCQ NSVRNAERRR ERMRNSQVWA

360 370 380 390 400
NGSCRTRSNG YANGGSVISH YHPTSNGNGN NNRHDTPQVT GRGSLHRNGP

410 420 430 440 450
PSPLNLQMTT FDSEIPLTFD QLPVSMESDR PLIEEMRSTS PPPPSGCLAR

460 470 480
FHPEAVDKFS IVAFPLAFTM FNLVYWWHYL SQTFDQNYQ

Fig. 3

MOD-1 is similar to ligand-gated ion channels

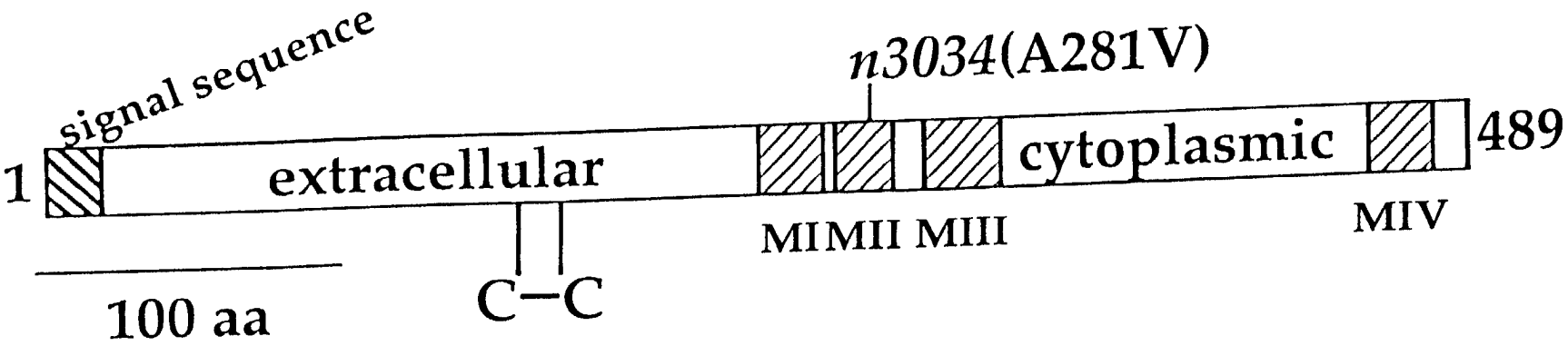

Fig. 4

ok103 is a 4135 bp deletion allele of *mod-1*

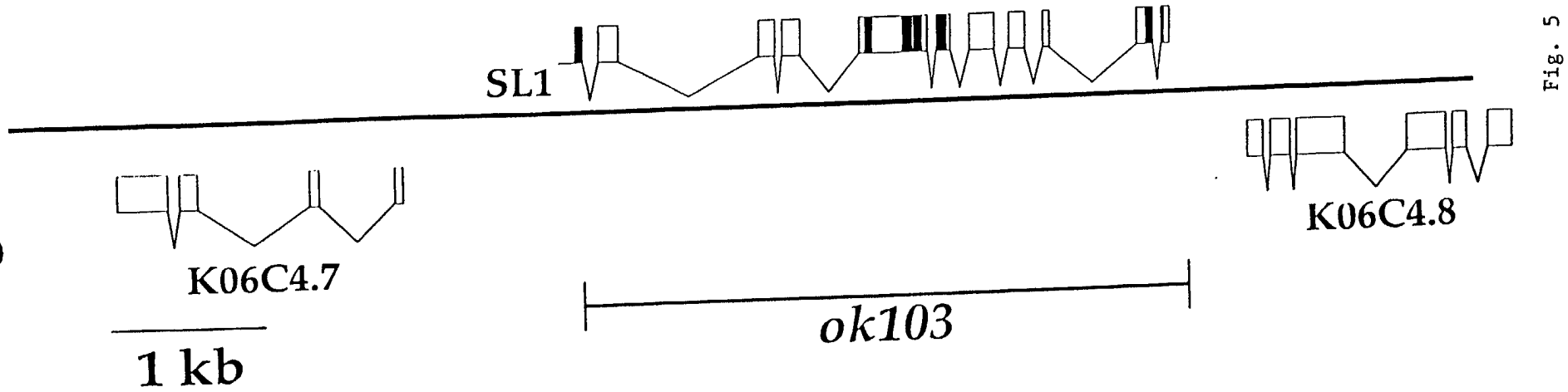

Fig. 5

10 20 30 40 50 60
TCATGTTTCA CGGAACGACG AATTTATCCC GTCGTTTCTT CCTTTCCGTT TTAACTCATA

70 80 90 100 110 120
TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTT GTTTTTTCGT

130 140 150 160 170 180
CGTTTAATTG TGGAAACACA TATCCGTCCT CTTTGAAACA GCATCAGAAA ACTTTCTGCT

190 200 210 220 230 240
CTCCGTGTCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACAACTAA

250 260 270 280 290 300
CTGCCAATGG GAGGAGCCAG TTGGAGCAGG GTGCGTGCTC GGTGCTCTTT TCAGAAGGTT

310 320 330 340 350 360
TTCTCTTGTG CCAGCATGCT TTTTTGAGGC TGTGTCATCA CAATGAACAT GTGTGAGTTC

370 380 390 400 410 420
ATCCGTCTGG ATTATTCTTT TTCTTACGTC TTCTGAGTAC TTCATACTTT CCAAATTTTT

430 440 450 460 470 480
CAACTGAACT TTTCTTCTTT TCTCATTGAA GTGGTTTGGT TTTGGTCGCG TGATCAACGG

490 500 510 520 530 540
ATCCTACTTT TTTGAAACAA AATGTTTTTG AAGTTTCACA GACTGATTTC GGGGTTTTTT

550 560 570 580 590 600
CAAAGAATAT ATTCCCTCTC GAGCAAGAGA AAATTCCAGA AAATAGTAGT TTTTTTCAAT

610 620 630 640 650 660
TAGTCGTTTC ATTTGTACTA GCTAAAAAAC TTGCAACTTA TGGCTTTAAA ACATGTGTTG

670 680 690 700 710 720
GCTTCATACA AAAACATTTA ACTAGTGTTT TTCCAGTTTT GTGTTCGTTT CATTTTCTCA

730 740 750 760 770 780
CCAAACTGAC AATAATTACT TTCTGTGAAC GTGTTTTGTA GGCAAGCTCC CGAATATTTT

790 800 810 820 830 840
TTTCTCTTCT CACGTCTTGT TATTTTCTCG ATTTTATTTT CTGAATCTGT GCGGTTTTCA

850 860 870 880 890 900
ATCAATTTGA TTGCGATAAT TATTCTATCA GAAATATATT TTCAGAAATC CAAATACTCC

910 920 930 940 950 960
AGGTGCCAAT GCGGTGAAAG AAAATTATGA AGTTTATTCC TGAAATCACA CTACTCTTGC

970 980 990 1000 1010 1020
TTTTATTTGT ACACTCTACA CAGGTTAGTT TCTCTTGAAT GTCCATTTTA ATATTTATAG

1030 1040 1050 1060 1070 1080
AACACTTTTA TGTACATTGT GTTGGTATTC AATTCGAAAA ACAATGAAAT TTATTTCTAA

1090 1100 1110 1120 1130 1140
ATAACTGCGT TTCTGGGGTT TCTATCAGCA CTTACTAGCT GACAAAAACT TTTCCGTATT

Fig. 6
Page 1

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      1150       1160       1170       1180       1190       1200
CGGAATTAGA TTTTTATGCA AGCAATGTTT CATTTTTACA CAGTATAGTA TTTATTCTTA

      1210       1220       1230       1240       1250       1260
CTTTTGATTA TATTGCTCGC ACCCTAAATG ACAGGTATTA GAAATTAACC GCTTTTCAGA

      1270       1280       1290       1300       1310       1320
GTATTTTTAA TCTTCTTAGT ACTAGTTTAG TTCTTTAAAT AAGAAACCAT CTAGTTTTTC

      1330       1340       1350       1360       1370       1380
ATTATCACTC AACTTCAGTC GGACAAATTT TAAATTTTTT ACTCGATAAA AAAATTTTAT

      1390       1400       1410
AATTCAGACA AATTATGTCT TCTCATTTTT GATCGCT
```

Fig. 6

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        10         20         30         40         50         60
TCATGTTTCA CGGAACGACG AATTTATCCC GTCGTTTCTT CCTTTCCGTT TTAACTCATA

        70         80         90        100        110        120
TCTCTTCCTG GATCCTTCAG AGCTCTTGTC AATTCCTCAC GTTTTTTTTT GTTTTTTCGT

       130        140        150        160        170        180
CGTTTAATTG TGGAAACACA TATCCGTCCT CTTTGAAACA GCATCAGAAA ACTTTCTGCT

       190        200        210        220        230        240
CTCCGTGTCC TTCTACTTAC TCTGATTGCC TTAGTTAGTC ACATCGCAAG CAACAACTAA

       250        260        270        280        290        300
CTGCCAATGG GAGGAGCCAG TTGGAGCAGG GTGCGTGCTC GGTGCTCTTT TCAGAAGGTT

       310        320        330        340        350        360
TTCTCTTGTG CCAGCATGCT TTTTTGAGGC TGTGTCATCA CAATGAACAT GTGTGAGTTC

       370        380        390        400        410        420
ATCCGTCTGG ATTATTCTTT TTCTTACGTC TTCTGAGTAC TTCATACTTT CCAAATTTTT

       430        440        450        460        470        480
CAACTGAACT TTTCTTCTTT TCTCATTGAA GTGGTTTGGT TTTGGTCGCG TGATCAACGG

       490        500        510        520        530        540
ATCCTACTTT TTTGAAACAA AATGTTTTTG AAGTTTCACA GACTGATTTC GGGGTTTTTT

       550        560        570        580        590        600
CAAAGAATAT ATTCCCTCTC GAGCAAGAGA AAATTCCAGA AAATAGTAGT TTTTTTCAAT

       610        620        630        640        650        660
TAGTCGTTTC ATTTGTACTA GCTAAAAAAC TTGCAACTTA TGGCTTTAAA ACATGTGTTG

       670        680        690        700        710        720
GCTTCATACA AAAACATTTA ACTAGTGTTT TTCCAGTTTT GTGTTCGTTT CATTTTCTCA

       730        740        750        760        770        780
CCAAACTGAC AATAATTACT TTCTGTGAAC GTGTTTTGTA GGCAAGCTCC CGAATATTTT

       790        800        810        820        830        840
TTTCTCTTCT CACGTCTTGT TATTTTCTCG ATTTTATTTT CTGAATCTGT GCGGTTTTCA

       850        860        870        880        890        900
ATCAATTTGA TTGCGATAAT TATTCTATCA GAAATATATT TTCAGAAATC CAAATACTCC

       910        920        930        940        950        960
AGGTGCCAAT GCGGTGAAAG AAAATTATGA AGTTTATTCC TGAAATCACA CTACTCTTGC

       970        980        990       1000       1010       1020
TTTTATTTGT ACACTCTACA CAGGTTAGTT GGTTGATTCT AGATCTCTTG CCTCCTAGCT

      1030       1040       1050       1060       1070       1080
TGCAAGGATA ATATAATTGA ATTGTTTTTG AGGAGTGCAA AGATTGAATA GTTTTCTATA

      1090       1100       1110       1120       1130       1140
TTTAGGCTAA AGGAAAACGA CGGAAATGTC CGGAGGGTGC GTGGTCGGAA GGAAAGATTA
```

Fig. 7

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      1150       1160       1170       1180       1190       1200
TGAACACGAT CATGAGCAAC TACACGAAAA TGTTGCCCGA CGCGGAGGAC AGCGTACAAG

      1210       1220       1230       1240       1250       1260
TTAATATTGA GATTCATGTA CAGGTTGGTA GACTCTATAA TTGCACACCA ATATGTGAAA

      1270       1280       1290       1300       1310       1320
GTTTTCTTTA AAATTAAACT GCTGTAAATG ACTTTTGAAT AAGTTTATCA GATAGAAATT

      1330       1340       1350       1360       1370       1380
GTCTGAACTT TTCGATTCAA ACTTTCCGAA CTTCAAAGCG GTTCCAAATT ACTCACTTCC

      1390       1400       1410       1420       1430       1440
ATTTATCTCT TTGCTACAAT TTCTCCCACA AAGCCTTTTT CTTCATTTAA CGTTCTTTTT

      1450       1460       1470       1480       1490       1500
TATGTCGTTG TTCTTACAAA CAATTTCGTC TCCTTGATGA ACTGCTTGAA CTGAGAATAG

      1510       1520       1530       1540       1550       1560
TCACATGAGG ATAAATTTGA TGGAATGACA AGTTTTGTGC CCAGAAGGCA GTTTTGCACT

      1570       1580       1590       1600       1610       1620
GAACTTGTTC AGTTGCAGAC ACATCTCAAA ACACAGAAGA TGAGTGGAAA ACTAGTGAGA

      1630       1640       1650       1660       1670       1680
GACTGCCAAA AGTCGAAGGG ATAATGAAAA TTTGTTGCAA ATGAATTCTG CGAAGTTATG

      1690       1700       1710       1720       1730       1740
TGAAAAATTA TTGGATTGGG AGTTGTGGGA GTGAAGAGAT GGGTCAAAAG CCATCAATCT

      1750       1760       1770       1780       1790       1800
TGAATGCTTC GGTCAAAGAT TTGTTTCTCA TATGTTTACA ACACTGAAAA CAATCTATCC

      1810       1820       1830       1840       1850       1860
TAGAAATGTT TGAACCACCC TCTAAAGTCC TTCCGTATAT TTTTTCATCT TTATACCGAC

      1870       1880       1890       1900       1910       1920
CAGAATTCAA GAGTTGTTTG AAATAACTTC CTCTTTTTTG GAGAATATGT ACTCAGATTT

      1930       1940       1950       1960       1970       1980
TTACATTCAA AATTTATATA TTTTCAAATA GAAAAAGTGC CAAGTACCAG AAACTTTTAT

      1990       2000       2010       2020       2030       2040
CAAGTTGGCG GCACTTTGGA GAGTGAATTT GATGAAAAAG TGTTTGATAA GTTTGTCGGG

      2050       2060       2070       2080       2090       2100
CAAACTGGTC CCCTGGGTGG GGAAATGGTG GCATTTTTGG AAACATTTTC ATAGTCGAAG

      2110       2120       2130       2140       2150       2160
AAGTGGAACA AGAAAATTGG AAAATAGAGA TACATATGTA TATGAAAATA GAATTGAACA

      2170       2180       2190       2200       2210       2220
GGAACTTATT TTTATTTTCA GGATATGGGA AGCTTGAATG AAATATCATC CGACTTTGAA

      2230       2240       2250       2260       2270       2280
ATTGACATTT TATTCACTCA ACTGTGGCAT GACTCGGCAC TTTCTTTTGC TCATCTTCCG
```

Fig. 7

2290 2300 2310 2320 2330 2340
GCTTGTAAGC GGTAAGAAAT CTTTGTATTA GAAGGGAAAA ATATTTAAAT TAATGAAATT

2350 2360 2370 2380 2390 2400
TCAGAAATAT CACAATGGAA ACACGACTTT TACCTAAGAT TTGGTCTCCA AACACGTGTA

2410 2420 2430 2440 2450 2460
TGATTAATTC AAAACGAACA ACCGTCCATG CATCACCATC GGAAAATGTG ATGGTTATTC

2470 2480 2490 2500 2510 2520
TGTACGAGGT ATGATTTTTG ATTTTGTGAC GTCACAAACA GAGCATGTCT AAGGGCATGT

2530 2540 2550 2560 2570 2580
TGTAGCAAGA AAAAAACGGA TTCTTGTCTC TGTCGACGTT TCCTAAGTAT TGTGAATTAT

2590 2600 2610 2620 2630 2640
TTATAATACA TCACTCTAAT TACGTGAATA CTTACACCTT TAACTGGGTG AAGGATAAAA

2650 2660 2670 2680 2690 2700
TAGAGAAGGA GACGTTGAAA AAGCTCTTCG GTAGATTAAA GAGTCTAGAA TCGACATATG

2710 2720 2730 2740 2750 2760
TATTCATGTT TCTCGGTTCA GGGAAATAAG TGATTTTGGC GAAAAAGAGT TAGACGACAT

2770 2780 2790 2800 2810 2820
TTTTTAGAAA ACTAAAACTA TATTCTCGAA CCCAAATCAG TCTAATGGTT TTCAGCAAAA

2830 2840 2850 2860 2870 2880
AGTATGAAAT ATACAATGTT TGTTTCAGAA TACCCAGTAC AAAATTTGAA GTTTTTCAGA

2890 2900 2910 2920 2930 2940
ATGGAACAGT CTGGATTAAC CATCGTCTTA GTGTCAAATC ACCTTGCAAT TTGGATCTGC

2950 2960 2970 2980 2990 3000
GACAGTTTCC TTTCGATACT CAAACTTGCA TATTAATCTT TGAATCCTAT AGTCATAACT

3010 3020 3030 3040 3050 3060
CAGAAGAAGT TGAACTTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG CCAATTCAAC

3070 3080 3090 3100 3110 3120
TTCCTGACTT TGATATGGTT CATTATTCAA CTAAAAAGGA AACTTTACTC TATCCAAACG

3130 3140 3150 3160 3170 3180
GGTACTGGGA TCAGCTTCAA GTTACTTTCA CTTTCAAACG ACGATATGGA TTCTATATTA

3190 3200 3210 3220 3230 3240
TTCAAGCCTA TGTTCCAACA TATCTTACAA TCATTGTATC TTGGGTTTCA TTCTGCATGG

3250 3260 3270 3280 3290 3300
AACCAAAAGC TCTGCCGGCA AGAACAACTG TCGGAATCTC ATCTCTTCTA GTTCTTACTT

3310 3320 3330 3340 3350 3360
TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA GGTTTGTTTT

3370 3380 3390 3400 3410 3420
TTTTCTTTTT CAAACAAATA AAAAAAAAGA TAAACAAATA TTTGTTTCAG CAATGGATGT

Fig. 7
Page 3

3430 3440 3450 3460 3470 3480
GTGGATGCTT GGATGCATAT CATTTGTCTT CGGAACCATG GTAGAATTGG CATTTGTTTG

3490 3500 3510 3520 3530 3540
TTACATTTCC CGTTGTCAGA ACAGCGTAAG AAAGTGAGTT GGCATAAGAG TTTTCTCACG

3550 3560 3570 3580 3590 3600
TGGAGGGAAG TAATTAAATT TTGGGTGTCA TATGAAAATA TCAAAAACAA TATCAGGAAA

3610 3620 3630 3640 3650 3660
TTGAATTTCA CTATGATTTC GTAGTAAACA AATTACAGCG CGGAACGACG ACGGGAACGA

3670 3680 3690 3700 3710 3720
ATGAGAAATT CTCAGGTGTG GGCAAACGGA TCGTGTAGAA CTAGAAGCAA CGGGTATGCA

3730 3740 3750 3760 3770 3780
AACGGGGGAT CTGTAATCTC ACATTATCAT CCAACAAGCA ATGGAAATGG GAATAATAAT

3790 3800 3810 3820 3830 3840
CGACATGATA CACCTCAAGT TACTGGAAGG TTAGCAATCT CTATGATAGC ATTTATCAAT

3850 3860 3870 3880 3890 3900
TATTAAAGAA CTCTGGAATT AGTTTTTAAA GTATAAATAA ATCTCTATTT CTTGCGACCT

3910 3920 3930 3940 3950 3960
ACATTGAACT TAATAGTTAT GTTTTACAGA GGATCACTTC ATCGAAACGG GCCACCATCT

3970 3980 3990 4000 4010 4020
CCATTAAACC TTCAAATGAC TACATTTGAT TCGGAGATCC CTCTGACTTT TGATCAGGTG

4030 4040 4050 4060 4070 4080
AGTCTTACAT TGAGTTCAAA CTTTTTGAAT TTAAGCGTTC TATCTGATAA AGTTCTTCGG

4090 4100 4110 4120 4130 4140
TGGTTTTATA ATTTTTGATT CATAAACTTA CCCACTCCTT TCTCACTAAC ATTTTACCCT

4150 4160 4170 4180 4190 4200
GTTCAGCTGC CAGTTTCCAT GGAATCCGAT AGACCCCTGA TTGAAGAGGT AACTGTGAAA

4210 4220 4230 4240 4250 4260
GTAGTCAATT AATTCCCTGT GTTTCTACCC CACTCAATCC TTTTGTATTT TTTGTTCAGT

4270 4280 4290 4300 4310 4320
CTATCCACTA TCAATGTCTT ATCACCTCTA GATACTGTTT AGAAGAAAAT ATTGTTCACA

4330 4340 4350 4360 4370 4380
GTTATGGAAA TCACATATAC TTTGTTCTGG AATTGTATAT GTATGCTTTG AAAAAGCACA

4390 4400 4410 4420 4430 4440
TTAGAATACT ACAAACATTA GTTTCCATCA GATTTTTGAT TTATCAAAAC CGTTATATTA

4450 4460 4470 4480 4490 4500
GACACTCTTA AGTTATCATA TTCTAATTTC CAAGAATGTT ATATTTTGAA GAAGCCGGTG

4510 4520 4530 4540 4550 4560
ATTGTCAAAA AGATTGAAAA CTCCGAGTTT CTATATATGC GAAATTTTCA CTTCAGCCCA

Fig. 7
Page 4

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      4570        4580        4590        4600        4610        4620
CACACACACA CACACATTCA CGAAACTTTG TGTTGTTTAT GTTACTTATA TGTTATCTTT

      4630        4640        4650        4660        4670        4680
TCTGTCTGAT CATGGTTTTC GGACTGAAAT TGTGTTAATC GGAAGTTATA TGTGAGCCAC

      4690        4700        4710        4720        4730        4740
ATTGATTAAA CCTGTGAGAG ATGCCCATTT GTACTCATTT TACGACTGTC TCATGTCCAA

      4750        4760        4770        4780        4790        4800
ACACCATGTT TATTGTAATT ACCAGGCTAC TATTTGCAGA TGCGATCAAC ATCACCACCT

      4810        4820        4830        4840        4850        4860
CCACCATCTG GATGTCTGGC CAGATTCCAT CCGGAAGCAG TGGACAAATT CTCCATTGTA

      4870        4880        4890        4900        4910        4920
GCTTTTCCAT TGGCATTTAC AATGTTTAAT GTTAGTTAAT CCACAGTTAA AAATTCCCAT

      4930        4940        4950        4960        4970        4980
AATCATAAAT ATCTCGACTT TTCAGCTTGT CTACTGGTGG CACTATTTGT CTCAAACTTT

      4990        5000        5010        5020        5030        5040
CGATCAAAAC TATCAGTGAT TGAAGTTTAT CCCTTTTAAT TCCAATAATT CACAGTTGCC

      5050        5060        5070        5080        5090        5100
GGTATCTACC TCCATTCTTT TCCGATGATT CGCAGTTTTT CACAGGGTTC AAATGTATCT

      5110        5120        5130        5140        5150        5160
CGTTCAATCT TTTTATGGTT ATTTCTCTTG AATGTCCATT TTAATATTTA TAGAACACTT

      5170        5180        5190        5200        5210        5220
TTATGTACAT TGTGTTGGTA TTCAATTCGA AAAACAATGA AATTTATTTC TAAATAACTG

      5230        5240        5250        5260        5270        5280
CGTTTCTGGG GTTTCTATCA GCACTTACTA GCTGACAAAA ACTTTTCCGT ATTCGGAATT

      5290        5300        5310        5320        5330        5340
AGATTTTTAT GCAAGCAATG TTTCATTTTT ACACAGTATA GTATTTATTC TTACTTTTGA

      5350        5360        5370        5380        5390        5400
TTATATTGCT CGCACCCTAA ATGACAGGTA TTAGAAATTA ACCGCTTTTC AGAGTATTTT

      5410        5420        5430        5440        5450        5460
TAATCTTCTT AGTACTAGTT TAGTTCTTTA AATAAGAAAC CATCTAGTTT TTCATTATCA

      5470        5480        5490        5500        5510        5520
CTCAACTTCA GTCGGACAAA TTTTAAATTT TTTACTCGAT AAAAAAATTT TATAATTCAG

      5530        5540        5550
ACAAATTATG TCTTCTCATT TTTGATCGCT
```

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        10         20         30         40         50         60
ATGAAGTTTA TTCCTGAAAT CACACTACTC TTGCTTTTAT TTGTACACTC TACACAGGCT

        70         80         90        100        110        120
AAAGGAAAAC GACGGAAATG TCCGGAGGGT GCGTGGTCGG AAGGAAAGAT TATGAACACG

       130        140        150        160        170        180
ATCATGAGCA ACTACACGAA AATGTTGCCC GACGCGGAGG ACAGCGTACA AGTTAATATT

       190        200        210        220        230        240
GAGATTCATG TACAGGATAT GGGAAGCTTG AATGAAATAT CATCCGACTT TGAAATTGAC

       250        260        270        280        290        300
ATTTTATTCA CTCAACTGTG GCATGACTCG GCACTTTCTT TTGCTCATCT TCCGGCTTGT

       310        320        330        340        350        360
AAGCGAAATA TCACAATGGA AACACGACTT TTACCTAAGA TTTGGTCTCC AAACACGTGT

       370        380        390        400        410        420
ATGATTAATT CAAAACGAAC AACCGTCCAT GCATCACCAT CGGAAAATGT GATGGTTATT

       430        440        450        460        470        480
CTGTACGAGA ATGGAACAGT CTGGATTAAC CATCGTCTTA GTGTCAAATC ACCTTGCAAT

       490        500        510        520        530        540
TTGGATCTGC GACAGTTTCC TTTCGATACT CAAACTTGCA TATTAATCTT TGAATCCTAT

       550        560        570        580        590        600
AGTCATAACT CAGAAGAAGT TGAACTTCAT TGGATGGAAG AAGCTGTCAC ATTAATGAAG

       610        620        630        640        650        660
CCAATTCAAC TTCCTGACTT TGATATGGTT CATTATTCAA CTAAAAAGGA AACTTTACTC

       670        680        690        700        710        720
TATCCAAACG GGTACTGGGA TCAGCTTCAA GTTACTTTCA CTTTCAAACG ACGATATGGA

       730        740        750        760        770        780
TTCTATATTA TTCAAGCCTA TGTTCCAACA TATCTTACAA TCATTGTATC TTGGGTTTCA

       790        800        810        820        830        840
TTCTGCATGG AACCAAAAGC TCTGCCGGCA AGAACAACTG TCGGAATCTC ATCTCTTCTA

       850        860        870        880        890        900
GTTCTTACTT TCCAGTTTGG AAATATTTTG AAAAATCTTC CAAGGGTTTC ATATGTGAAA

       910        920        930        940        950        960
GCAATGGATG TGTGGATGCT TGGATGCATA TCATTTGTCT TCGGAACCAT GGTAGAATTG

       970        980        990       1000       1010       1020
GCATTTGTTT GTTACATTTC CCGTTGTCAG AACAGCGTAA GAAACGCGGA ACGACGACGG

      1030       1040       1050       1060       1070       1080
GAACGAATGA GAAATTCTCA GGTGTGGGCA AACGGATCGT GTAGAACTAG AAGCAACGGG

      1090       1100       1110       1120       1130       1140
TATGCAAACG GGGGATCTGT AATCTCACAT TATCATCCAA CAAGCAATGG AAATGGGAAT
```

Fig. 8
Page 1

1150	1160	1170	1180	1190	1200
AATAATCGAC	ATGATACACC	TCAAGTTACT	GGAAGAGGAT	CACTTCATCG	AAACGGGCCA
1210	1220	1230	1240	1250	1260
CCATCTCCAT	TAAACCTTCA	AATGACTACA	TTTGATTCGG	AGATCCCTCT	GACTTTTGAT
1270	1280	1290	1300	1310	1320
CAGCTGCCAG	TTTCCATGGA	ATCCGATAGA	CCCCTGATTG	AAGAGATGCG	ATCAACATCA
1330	1340	1350	1360	1370	1380
CCACCTCCAC	CATCTGGATG	TCTGGCCAGA	TTCCATCCGG	AAGCAGTGGA	CAAATTCTCC
1390	1400	1410	1420	1430	1440
ATTGTAGCTT	TTCCATTGGC	ATTTACAATG	TTTAATCTTG	TCTACTGGTG	GCACTATTTG
1450	1460	1470			
TCTCAAACTT	TCGATCAAAA	CTATCAGTGA			

Fig. 8
Page 2

Fig. 9a

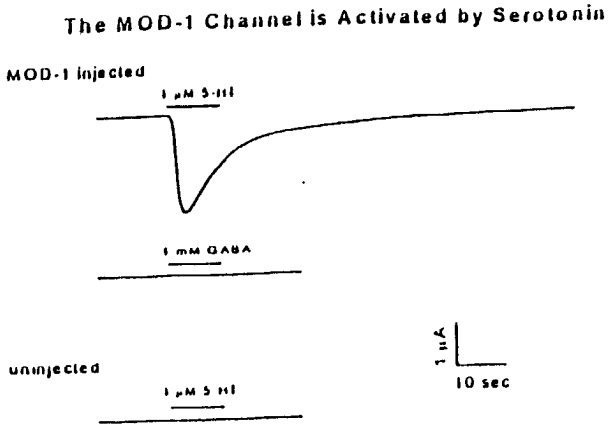


Fig. 9b

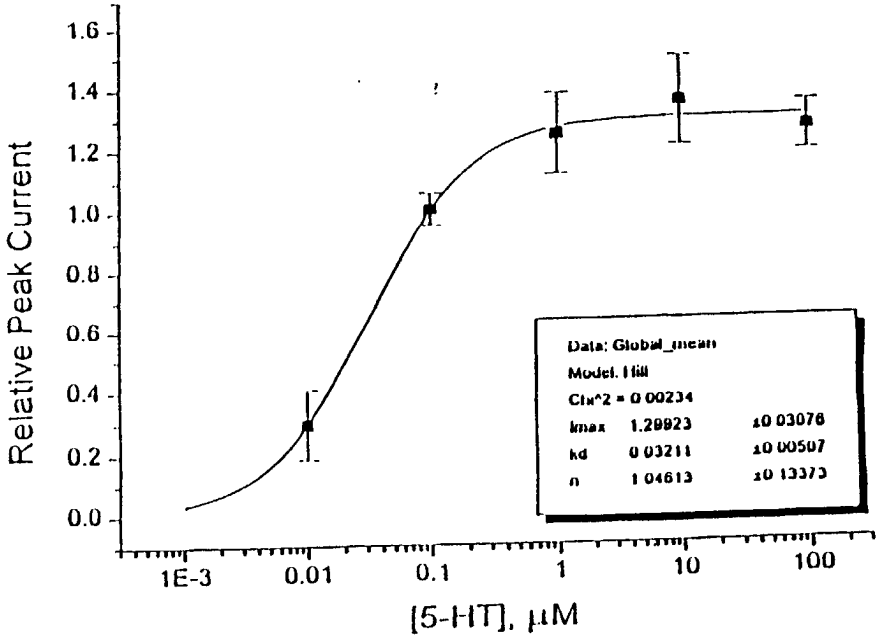


Fig. 9c

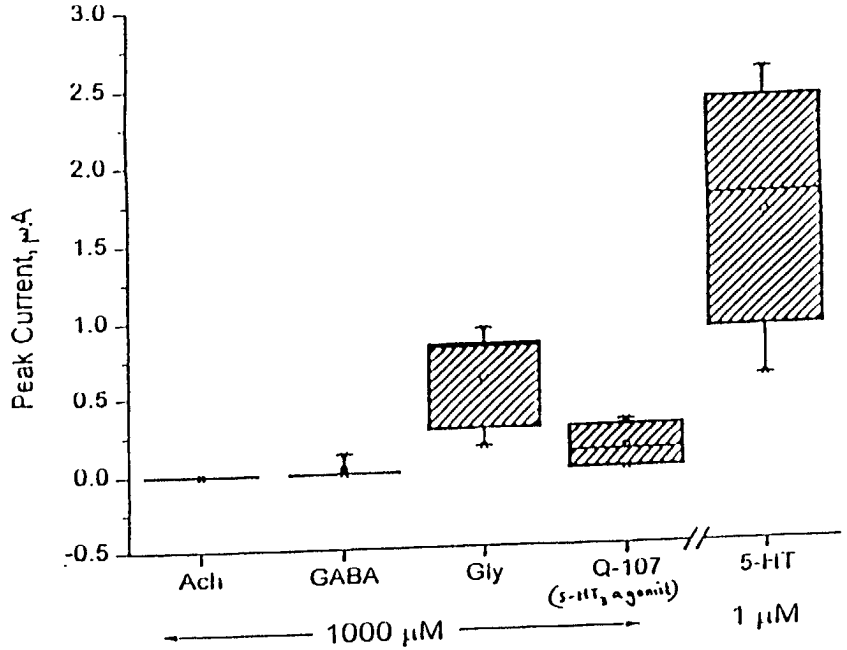


Fig. 9

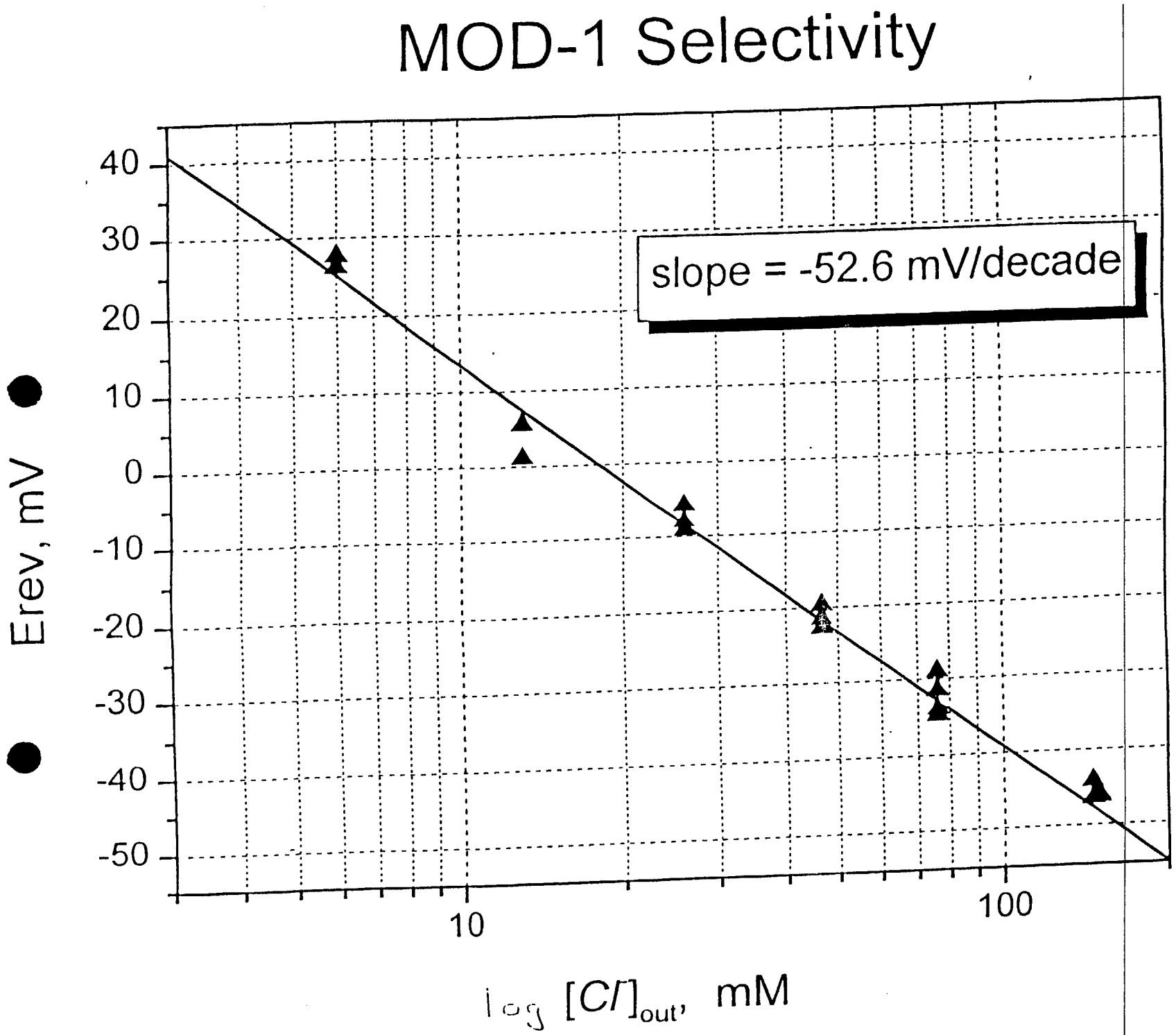


Fig. 10

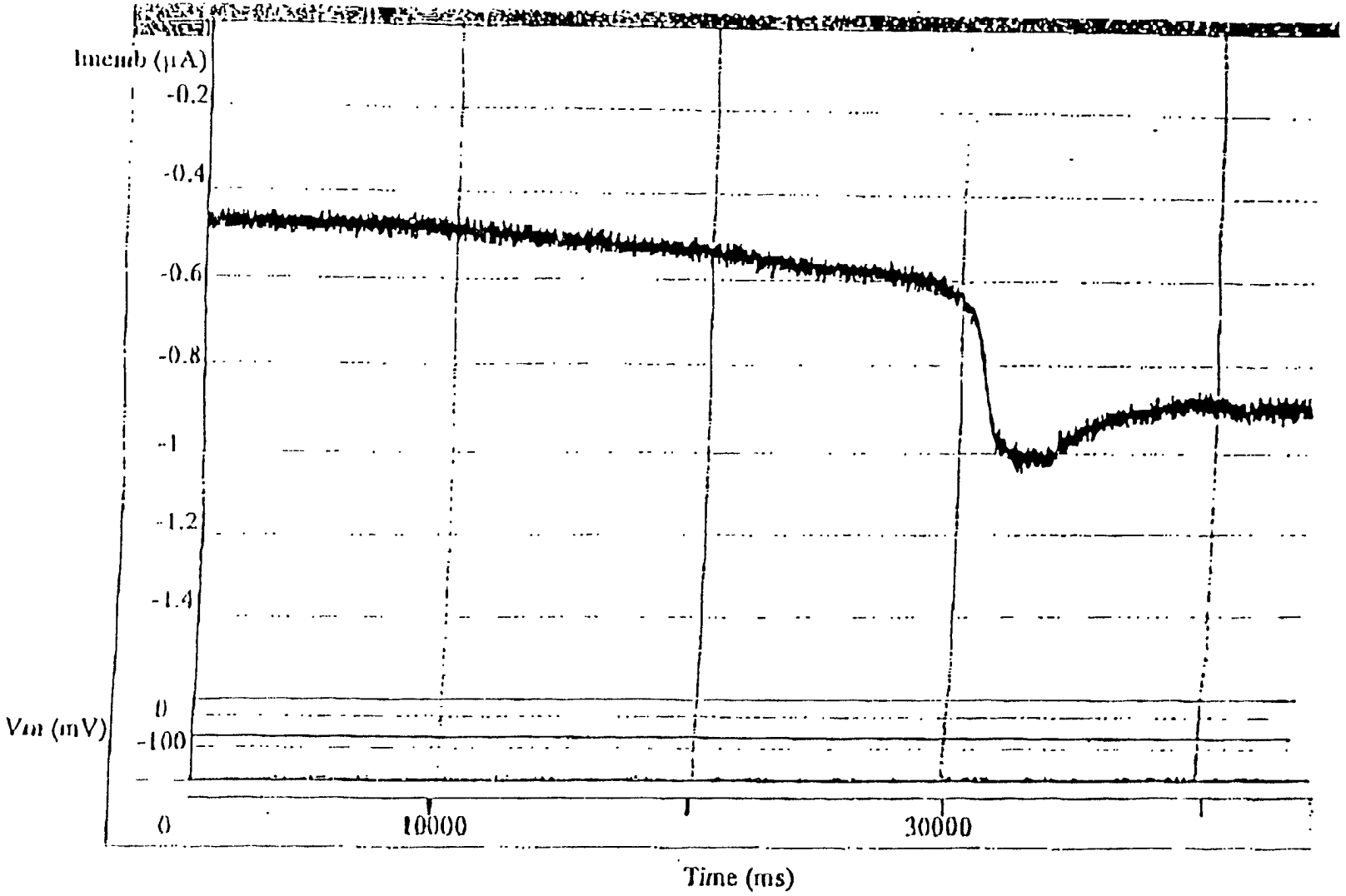
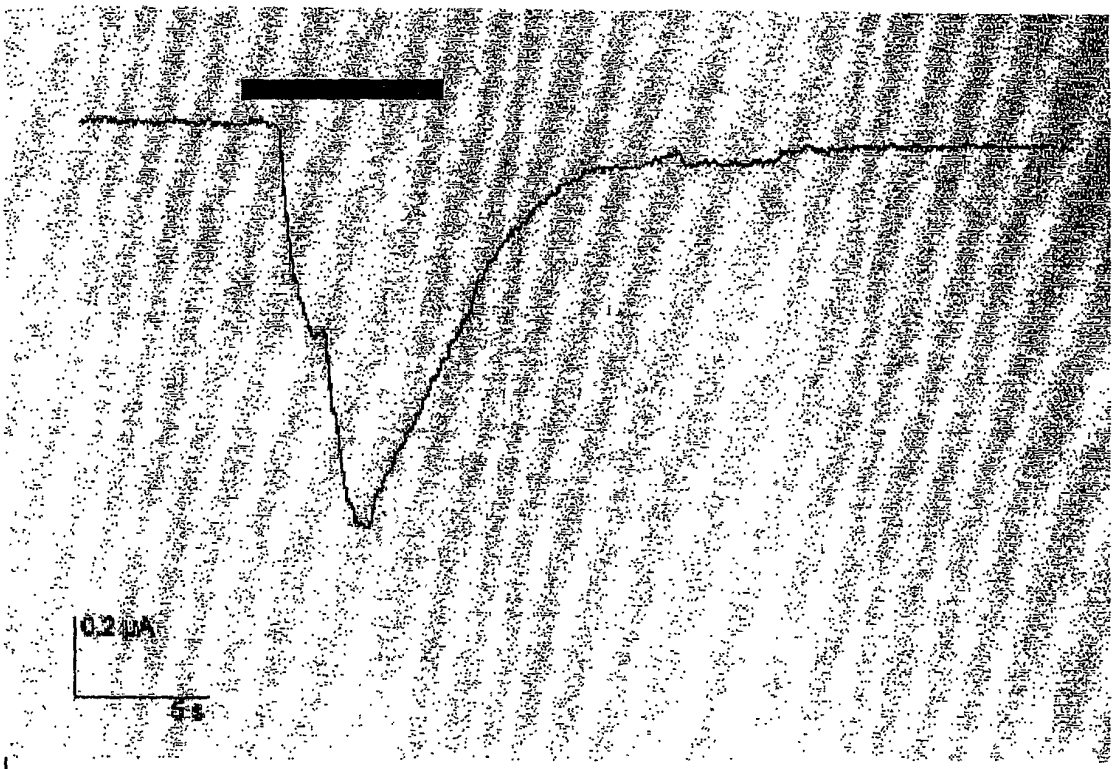


Figure 11

04/01/2000



Oocyte injected with rat cortex poly(A)+ RNA.
Membrane potential -70 mV. 1 μM 5-HT applied (bar)
Oocyte was pretreated with 0.2 mM BAPTA-AM for 2 hours.
The bath solution contained 2 mM Co^{2+} to block 5-HT3a responses.

Fig. 12

PATENT
ATTORNEY DOCKET NO: 01997/521003

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled A NOVEL SEROTONIN-GATED ANION CHANNEL, the specification of which

- ■ is attached hereto.
- ☐ was filed on_____ as Application Serial No. _____ and was amended on _____.
- ☐ was described and claimed in PCT International Application No. _____ filed on _____ and as amended under PCT Article 19 on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56(a).

FOREIGN PRIORITY RIGHTS: I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

Country	Serial Number	Filing Date	Priority Claimed?
			Yes/No

PROVISIONAL PRIORITY RIGHTS: I hereby claim priority benefits under Title 35, United States Code, §119(e) and §120 of any United States provisional patent application(s) listed below filed by an inventor or inventors on the same subject matter as the present application and having a filing date before that of the application(s) of which priority is claimed:

Serial Number	Filing Date	Status
60/131,149	April 27, 1999	Pending

NON-PROVISIONAL PRIORITY RIGHTS: I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by

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the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose all information I know to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Serial Number	Filing Date	Status
09/559,622	April 27, 2000	Pending

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Paul T. Clark, Reg. No. 30,162, Karen L. Elbing, Ph.D., Reg. No. 35,238, Kristina Bieker-Brady, Ph.D., Reg. No. 39,109, Susan M. Michaud, Ph.D., Reg. No. 42,885, Mary Rose Scozzafava, Ph.D., Reg. No.36,268, James D. DeCamp, Ph.D., Reg. No. 43,580.

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

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01997.521003 Declaration and Power of Attorney.wpd